

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 12:57:07 ; Search time 7154 Seconds
(without alignments)
10881.198 Million cell updates/sec

Title: US-09-997-131-19

Perfect score: 1796

Sequence: 1 ggaagaggaagtccaagg.....aaaaaaaaagggcgccgc 1796

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
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- 30: em.htg.hum.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.tgo.hum.*
- 40: em.tgo.mus.*
- 41: em.tgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1792.8	99.8	1796	6	BD249816
2	1741.6	97.0	1837	6	AX358786 Sequence
3	1741.6	97.0	1837	6	AX362279 Sequence
4	1741.6	97.0	1837	9	AY358545 Homo sapi
5	1732.6	96.5	1747	6	AX083513 Sequence
6	1666.2	92.8	1785	6	AX747710 Sequence
7	1666.2	92.8	1785	9	AK092757 Homo sapi
8	1658.6	92.3	1696	9	AF251706 Homo sapi
9	1384.8	77.1	1923	9	BC028199 Homo sapi
10	948.8	52.8	956	9	AY303545 Homo sapi
11	920.6	51.3	163597	9	AC015888 Homo sapi
12	880.6	49.0	996	9	AF375480 Homo sapi
13	603	33.6	860	9	AF375481 Homo sapi
14	465.4	25.9	516	6	BD058338 Secretd
15	425.6	23.7	2559	6	AX458365 Sequence
16	414.6	23.1	431	6	AX370900 Sequence
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43	178.6	9.9	266770	2	AC130136 Rattus no
44	178.6	9.9	282163	2	AC113669 Rattus no
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ALIGNMENTS

RESULT 1
BD249816
LOCUS 33 human secreted proteins.
DEFINITION BD249816
ACCESSION BD249816.1 GI:33059586
VERSION JP 2002540763-A/18.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1796)
AUTHORS Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R., Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and Komatsoulis,G.

1796 bp DNA linear PAT 17-JUL-2003

QY 1501 ACAAGGGTCTCTATAGAAAGAGCGCCAGAGGTCACAAAGAGGTAGACACAAAGTGTATG 1560
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RESULT 2
 AX358786 1837 bp DNA linear PAT 13-FEB-2002
 LOCUS AX358786 Sequence 39 from Patent.W00193983.
 DEFINITION AX358786
 ACCESSION AX358786
 VERSION AX358786.1 GI:18675294
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Baker,K.P., Desnovers,L., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
 Watanabe,C.K. and Wood,W.I.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 Patent: WO 0193983-A 39 13-DEC-2001;
 Genentech Inc. (US)
 Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
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 ORIGIN
 Query Match 97.0%; Score 1741.6; DB 6; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 QY 32 ACCAGCAGAGGCTGGAGTCTGATGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAC 91
 Db 1 ACCAGCAGAGGCTGGAGTCTGATGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAC 60
 QY 92 GGGGACCTGTCTGAAGAGAAGATGCCCTGTGTGACACTCTACCTGCTCTCTTCTGGCTC 151
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 QY 452 GGAATGACCTTGGGTTCAGAGTTCAGTGAACATGACCCAGACACAGTCCACCAAGAA 511
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 QY 512 GAACTAGCAGTCTCCCAACTCTGACCGGCCACCACTTTGGAACAAGCACAAGTCTCTG 571
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 QY 632 TCACCTCTTGGCTTGGAGGATGATGAAGTACCAGAGAAAGCAGCGGATGTCCCCAGAG 691
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 QY 692 CAGGTACTGACGCTCTGGAGGCGACCTCTGCTATGACAGACCTGACCTCGAGTGGCC 751
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RESULT 3
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LOCUS Sequence 39 from Patent WO0208288.
DEFINITION AX362279
ACCESSION AX362279
VERSION AX362279.1 GI:18694597
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 39 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 97.0%; Score 1741.6; DB 6; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAGCGTGGAGTCTGTAGTTGTCTCTGCTGCCAGGCTCCACTGAGGGGAC 91
Db 1 ACCAGCAGAGCGTGGAGTCTGTAGTTGTCTCTGCTGCCAGGCTCCACTGAGGGGAC 60
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1321

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1741

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RESULT 4

AY358545

LOCUS

AY358545

DEFINITION

Homo sapiens clone DNA125200 PIGR (UNQ3105) mRNA, complete cds.

ACCESSION

AY358545

VERSION

AY358545.1

KEYWORDS

FLI CDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1837)

AUTHORS

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Curreli,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,J., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandien,R., Watanabe,C., Wileand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

TITLE

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

JOURNAL

Genome Res. 13 (10), 2265-2270 (2003)

PUBMED

12975309

REFERENCE

2 (bases 1 to 1837)

AUTHORS

Clark,H.F.

TITLE

Direct Submission

JOURNAL

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES

Location/Qualifiers

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97.0%; Score 1741.6; DB 9; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Mismatches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

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DEFINITION Sequence 55 from Patent WO0112662.
ACCESSION AX083513
VERSION AX083513.1 GI:13185323
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 Lal, P., Yue, H., Tang, Y.T., Bandman, O., Burford, N., Azimzai, Y.,
Baughn, M.R., Lu, D.A. and Patterson, C.
TITLE Membrane associated proteins
JOURNAL Patent: WO 0112662-A 55 22-FEB-2001;
Incyte Genomics, Inc. (US)
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Best Local Similarity 99.8%; Pred. No. 0;
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ACCESSION AX747710
 VERSION AX747710.1 GI:32132098
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Isegai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Iehii,S.,
 Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
 Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
 Masuko,Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1308459-A 1235 07-MAY-2003;
 Helix Research Institute (JP); Research Association for
 Biotechnology (JP)
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 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM
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 REFERENCE
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 AUTHORS
 Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaera, H., Furuya, T., Takahashi, M., Kikkawa, B., Onura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yanazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
 TITLE
 NEDO human cDNA sequencing project
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 1785)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 COMMENT
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Query Match 92.8%; Score 1666.2; DB 9; Length 1785;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1729; Conservative 8; Mismatches 1; Indels 47; Gaps 2;
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Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Schaez,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., McKernan,K.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1923)
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laxic,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripoop,S., Thomas,P.J., Touchman,J.W., Tsurgon,C., Vost,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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DEFINITION Homo sapiens chromosome 17, clone RP11-45215, complete sequence.
ACCESSION  AC016888
VERSION     AC016888.23  GI:27657593
KEYWORDS   HTG
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 163597)
AUTHORS   Birren,B., Nussbaum,C. and Lander,E.
TITLE     Homo sapiens chromosome 17, clone RP11-45215
JOURNAL   Unpublished
AUTHORS   2 (bases 1 to 163597)
AUTHORS   Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Farreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 163597)
Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cooke,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Farro,S., Farreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Mathews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

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JOURNAL   Submitted (15-DEC-2002) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS   4 (bases 1 to 163597)
AUTHORS   Birren,B., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
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Farro,S., Farreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Mathews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
JOURNAL   Submitted (12-JAN-2003) Whitehead Institute/MIT Center for Genome
REFERENCE Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Jan 12, 2003 this sequence version replaced gi:2665774.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5094
Center clone name: 452_I_5
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Only the last 163.6 kilobases of this clone are being submitted.
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DEFINITION
Sequence 36 from Patent WO0246385.
ACCESSION  AX458365
VERSION     AX458365.1  GI:211725037
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Tang,Y.T., Griffin,J.A., Yue,H., Lee,S.A., Baughn,M.R.,
Duggan,B.M., Walla,N.K., Lee,S., Ramkumar,J., Warren,B.A.,
Gandhi,A.R., Lu,D.A., Lu,Y., Yao,M.G., Ding,L., Tribouley,C.M.,
Sanjarwalla,M.M., Arvizu,C. and Hillman,J.L.
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Patent: WO 0246385-A 36 13-JUN-2002;
Incyte Genomics, Inc. (US)
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FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 12:52:57 ; Search time 740 Seconds
(without alignments)

10310.492 Million cell updates/sec

Title: US-09-997-131-19

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124098041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1741.6	97.0	1837	6 ABK3355	ABK3355 CDNA enco
3	1741.6	97.0	1837	7 ACA6860	ACA6860 CDNA enco
4	1741.6	97.0	1837	7 ACD68612	ACD68612 Novel hum
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ALIGNMENTS

RESULT 1

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ID AAC55198 standard; cDNA; 1796 BP.

XX AAC55198;

DT 16-JAN-2001 (first entry)

XX Human secreted protein gene 9 SEQ ID NO:19.

XX Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
antiparasitic; neuroprotective; nontropic; antiinflammatory; anti-HIV;
antitumor; antidiabetic; antihypertensive; diagnosis; immune disorder; AIDS;
agammaglobulinemia; haematopoietic cell disorder; blood protein disorder;
cardiovascular disorder; hyperproliferative disease; Gaucher's disease;
arrhythmia; ischaemia; congenital heart defect; pulmonary atresia;
atherosclerosis; neurological disease; Alzheimer's disease;
Huntington's chorea; infectious disease; cat-scratch disease; SS.

XX Homo sapiens.

XX WO200047602-A1.

PD 17-AUG-2000.

PF 08-FEB-2000; 2000WO-US003062.

PR 10-FEB-1999; 99US-0119468P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Roser CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;

PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;

DR WPI; 2000-543578/49.

DR P-PSDB; AAB32379.

XX New human nucleic acids encoding secreted proteins, useful in the
treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
diseases), blood protein disorders and hyperproliferative diseases (e.g.
Gaucher's disease).

PS Claim 1; Page 396-397; 488pp; English.

XX

CC The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic; immunostimulant
CC ; antiproliferative; cardiant; antiarrhythmic; antiviral; antibacterial;
CC antifungal; anticancer; neuroprotective; nontoxic; antiinflammatory;
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary aresia, arrhythmias, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention
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Query Match 99.8%; Score 1792.8; DB 3; Length 1796;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 TGACACTTACTGGTGGTAATGAAAACTGGAATGACCTTGGGTGACAGTCAAGT 480
DB 421 TGACACTTACTGGTGGTAATGAAAACTGGAATGACCTTGGGTGACAGTCAAGT 480

QY 481 GACCAATTGACCCAGCAGCTCACCAGAGAACTAGCAGCTCCCAACTCTGACCGG 540
DB 481 GACCAATTGACCCAGCAGCTCACCAGAGAACTAGCAGCTCCCAACTCTGACCGG 540

QY 541 CCACACTTGAACAACAGGCAACAGCTCTTGAAGCTCAGTGTCTCTGCTCCCTCATCTT 600
DB 541 CCACACTTGAACAACAGGCAACAGCTCTTGAAGCTCAGTGTCTCTGCTCCCTCATCTT 600

QY 601 CACCATATTCTGTGTTTGGTGGCGCTCACTCTTGGCTTGGAGGATGATGAAGTA 660
DB 601 CACCATATTCTGTGTTTGGTGGCGCTCACTCTTGGCTTGGAGGATGATGAAGTA 660

QY 661 CCAGCAGAAAGCAGCGGGATGTCCTCCAGCAGAGTACTCAGCCCTGGAGGGCAGCT 720
DB 661 CCAGCAGAAAGCAGCGGGATGTCCTCCAGCAGAGTACTCAGCCCTGGAGGGCAGCT 720

QY 721 CTGCTATGAGACCTTGACCTGCAGCTGGCCGGAACCTCCCGCGAAAGGCTTACCACGAA 780
DB 721 CTGCTATGAGACCTTGACCTGCAGCTGGCCGGAACCTCCCGCGAAAGGCTTACCACGAA 780

QY 781 GCTTTCTCTGCGCAGGTGACAGGTGGAAGTGAATATGTCACCATGGCTTCTTGGC 840
DB 781 GCTTTCTCTGCGCAGGTGACAGGTGGAAGTGAATATGTCACCATGGCTTCTTGGC 840

QY 841 GAAGAGGACATTTCTCTATGCACTCTGACCTTGGTGTGAGGATCAGGAACCGACCTA 900
DB 841 GAAGAGGACATTTCTATGCACTCTGACCTTGGTGTGAGGATCAGGAACCGACCTA 900

QY 901 CTGCAACATGGGCGCACTCAGTAGCCAMCTYCCCGCAGGGGCCCTGAGGAGCCACCGA 960
DB 901 CTGCAACATGGGCGCACTCAGTAGCCAMCTYCCCGCAGGGGCCCTGAGGAGCCACCGA 960

QY 961 ATACAGCACCATCAGCAGCCCTTAGCTGCACTCCAGGCTCTTCTTGACCCCGAGGCTG 1020
DB 961 ATACAGCACCATCAGCAGCCCTTAGCTGCACTCCAGGCTCTTCTTGACCCCGAGGCTG 1020

QY 1021 TGAGCACACTCTGCTCATCGACCTCTGCCCTCTGCCCTCATCAGGACCAACCG 1080
DB 1021 TGAGCACACTCTGCTCATCGACCTCTGCCCTCTGCCCTCATCAGGACCAACCG 1080

QY 1081 GGGACTGGTGGCTCTGCTGATCAGCAGCATTCGCCCTAGCTCTGGGTTGGGCTTGGG 1140
DB 1081 GGGACTGGTGGCTCTGCTGATCAGCAGCATTCGCCCTAGCTCTGGGTTGGGCTTGGG 1140

QY 1141 CCAAGTCTCAGGGGCTTCTAGGAGTTGGGTTTTCTAAAGTCCCTCTCTTACATA 1200
DB 1141 CCAAGTCTCAGGGGCTTCTAGGAGTTGGGTTTTCTAAAGTCCCTCTCTTACATA 1200

QY 1201 GTTGAAGGGGGCTTAGGATATGCTCTGGGGCTTCTAGGAGTGAAGATGATAT 1260
DB 1201 GTTGAAGGGGGCTTAGGATATGCTCTGGGGCTTCTAGGAGTGAAGATGATAT 1260

QY 1261 GAGAAAAATGTTATCATTTATCATGAAGTACCATTTATCATATACATCAATCACTTAT 1320
DB 1261 GAGAAAAATGTTATCATTTATCATGAAGTACCATTTATCATATACATCAATCACTTAT 1320

QY 1321 TTATTCCTTACCATGATGTTATGGCTGAATTAATGGCCCCCAAGATATCTGTGCTTAT 1380
DB 1321 TTATTCCTTACCATGATGTTATGGCTGAATTAATGGCCCCCAAGATATCTGTGCTTAT 1380

QY 1381 CCTCAGAACTTGTGACTGTACCTTCTGTGCGAAGAGGACAGTGCAGATGATGTAAG 1440
DB 1381 CCTCAGAACTTGTGACTGTACCTTCTGTGCGAAGAGGACAGTGCAGATGATGTAAG 1440

QY 1441 TTAAGGACTTTGAGATAGAGGTTTATTTCTGCTGATTCAGGTGGGCCCAAAATATCACC 1500
DB 1441 TTAAGGACTTTGAGATAGAGGTTTATTTCTGCTGATTCAGGTGGGCCCAAAATATCACC 1500

QY 1501 ACAAGGCTCTCATGAAGAGGCGCAGAGTCAAGAGGTAGAGTGAAGTGAAGTGAAGT 1560
DB 1501 ACAAGGCTCTCATGAAGAGGCGCAGAGTCAAGAGGTAGAGTGAAGTGAAGTGAAGT 1560

QY 1561 GAAAGTGGACGCTGGGTGTGACCTGAGCAGGGGCCATGAATGCGGAGCTTCAGATGCCAG 1620
DB 1561 GAAAGTGGACGCTGGGTGTGACCTGAGCAGGGGCCATGAATGCGGAGCTTCAGATGCCAG 1620

QY 1621 AAAGGGAAGGAATGGAATTCCTGCTGGAGCTCTCAAAGAAACCGCCCTCCACAG 1680
DB 1621 AAAGGGAAGGAATGGAATTCCTGCTGGAGCTCTCAAAGAAACCGCCCTCCACAG 1680

QY 1681 CTTGACTTGAAGCCATTGAACTGATCTTGGCTCTCAGATCTCAGATTCAGAGGAA 1740
DB 1681 CTTGACTTGAAGCCATTGAACTGATCTTGGCTCTCAGATCTCAGATTCAGAGGAA 1740

QY 1741 TAAATTTGTGTTGTTTAAATGAAAAAATAAAAAAAAAAAAAAAAAAGGGGGCGC 1796
DB 1741 TAAATTTGTGTTGTTTAAATGAAAAAATAAAAAAAAAAAAAAAAAAGGGGGCGC 1796

RESULT 2

ABK33555
ID ABK33555 standard; cDNA; 1837 BP.
XX
AC ABK33555;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 39.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; Gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 08-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI P-PSDB; AAU83611.
XX
DR WPI; 2002-172001/22.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 2; Fig 39; 359pp; English.

XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumors, especially lung
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
CC liver tumor. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells for stimulating
CC the proliferation or differentiation of chondrocyte cells, for

CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33556-ABK33657 represent human PRO
CC protein coding sequences of the invention
XX

SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 6; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY	32	ACCAGCAGAAGCTGGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGAAC	91
DB	1	ACCAGCAGAAGCTGGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGAAC	60
QY	92	GGGACCTGTCTGAAGAGAAGATGCCCTCTGCTGACACTCTACCTGCTCTTCTGGCTC	151
DB	61	GGGACCTGTCTGAAGAGAAGATGCCCTCTGCTGACACTCTACCTGCTCTTCTGGCTC	120
QY	152	TCAGGCTACTCTCATTTGCCACTCAAAATCACCGTCCACACACAGTGAATGGCTTGGAGCG	211
DB	121	TCAGGCTACTCTCATTTGCCACTCAAAATCACCGTCCACACACAGTGAATGGCTTGGAGCG	180
QY	212	GGCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	271
DB	181	GGCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	240
QY	272	TGTCAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACACAGTGGTGGTGGTGG	331
DB	241	TGTCAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACACAGTGGTGGTGGTGG	300
QY	332	GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACTTCACTGTG	391
DB	301	GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACTTCACTGTG	360
QY	392	ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTTGGTGTGAAATGAGAAAACT	451
DB	361	ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTTGGTGTGAAATGAGAAAACT	420
QY	452	GGAAATGACCTTGGGGTCAAGTTCAGTCAAGTCAAGTTCAGTCAAGTTCAGTCAAGTTC	511
DB	421	GGAAATGACCTTGGGGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTTC	480
QY	512	GAAATGACCTTGGGGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTTC	571
DB	481	GAAATGACCTTGGGGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTCAAGTTCAGTTC	540
QY	572	AAGTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	631
DB	541	AAGTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	600
QY	632	TCAGTCTTGGTGGAGGATGTAAGTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	691
DB	601	TCAGTCTTGGTGGAGGATGTAAGTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA	660
QY	692	CAGTCTAGCAAGCTTGGAGGCGACCTCTGCTATGACAGACCTGACCTGACCTGACCTG	751
DB	661	CAGTCTAGCAAGCTTGGAGGCGACCTCTGCTATGACAGACCTGACCTGACCTGACCTG	720
QY	752	GGACCTTCCCGGCAAGGCTACCAAGCAAGCTTCTCTGCGGCAAGCAAGCAAGCAAGCA	811
DB	721	GGACCTTCCCGGCAAGGCTACCAAGCAAGCTTCTCTGCGGCAAGCAAGCAAGCAAGCA	780
QY	812	GTGGAATATGTACCATGGTTCCTTCCGCAAGGAGGACATTTCTTATGCATCTCTGACC	871
DB	781	GTGGAATATGTACCATGGTTCCTTCCGCAAGGAGGACATTTCTTATGCATCTCTGACC	840
QY	872	TTGGGTCTCAGGATCAGGACCGACTCTGCAATGCGGCAAGCTCAGTACGCACTCT	931
DB	841	TTGGGTCTCAGGATCAGGACCGACTCTGCAATGCGGCAAGCTCAGTACGCACTCT	900

QY 392 ACCATGGAGGATCTCATGAAACTGATGCTGACACCTTACTGGTGTGGAATTGAGAAACT 451
Db 361 ACCATGGAGGATCTCATGAAACTGATGCTGACACCTTACTGGTGTGGAATTGAGAAACT 420
QY 452 GGAATGACCTTGGGTCACAGTTCAAGTGAACCATTCACCCAGCACCAGTCAACCAAGAA 511
Db 421 GGAATGACCTTGGGTCACAGTTCAAGTGAACCATTCACCCAGCACCAGTCAACCAAGAA 480
QY 512 GAAACTAGACGCTCCCAACTCTGACCGGACACCATTTGAGCAACAGGCAACAGCTCTTG 571
Db 481 GAAACTAGACGCTCCCAACTCTGACCGGACACCATTTGAGCAACAGGCAACAGCTCTTG 540
QY 572 AAGCTCAGTCCTCCCTGCGCCCTCATCTTCAACATATTKYTGCTTTGGTGGCGCC 631
Db 541 AAGCTCAGTCCTCCCTGCGCCCTCATCTTCAACATATTTGCTTGGTGGCGCC 600
QY 632 TCACTCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCCCAGAG 691
Db 601 TCACTCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCCCAGAG 660
QY 692 CAGTACTGACGCTCCCTGAGGGGACCTCTGCTATGACAGACCTGACCTGACGCTGGCC 751
Db 661 CAGTACTGACGCTCCCTGAGGGGACCTCTGCTATGACAGACCTGACCTGACGCTGGCC 720
QY 752 GGAACCTCCCGGAAAGGCTTACCACGAAGCTTTCTCTGCCACAGTTGACCAAGTGAA 811
Db 721 GGAACCTCCCGGAAAGGCTTACCACGAAGCTTTCTCTGCCACAGTTGACCAAGTGAA 780
QY 812 GTGGAATATGTCACATGGCTTCTTGGCAGAGGAGACATTTCTATGATCTGTGACC 871
Db 781 GTGGAATATGTCACATGGCTTCTTGGCAGAGGAGACATTTCTATGATCTGTGACC 840
QY 872 TTGGTGTCTGAGGATCAGGAACCGACCTACTGCAACATGGCCAMCTCAGTAGCCACTY 931
Db 841 TTGGTGTCTGAGGATCAGGAACCGACCTACTGCAACATGGCCAMCTCAGTAGCCACTY 900
QY 932 CCGGCGAGGGCCCTGAGGAGCCACCGAATACAGCACCATCAGCAGGCGCTTAGCCCTGCA 991
Db 901 CCGGCGAGGGCCCTGAGGAGCCACCGAATACAGCACCATCAGCAGGCGCTTAGCCCTGCA 960
QY 992 CTCAGGCTCTTCTTGGACCCAGGCTGTGAGCACHACTCTGCTCATGACCGCTGTC 1051
Db 961 CTCAGGCTCTTCTTGGACCCAGGCTGTGAGCACHACTCTGCTCATGACCGCTGTC 1020
QY 1052 CCCCTGTCTCCCTCATCAGGACCAACCCGGGACTGGTCTGCTCTGATCAGCCAGCA 1111
Db 1021 CCCCTGTCTCCCTCATCAGGACCAACCCGGGACTGGTCTGCTCTGATCAGCCAGCA 1080
QY 1112 TTGCCCTTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGG 1171
Db 1081 TTGCCCTTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGG 1140
QY 1172 TTTTCTAAAGCTCCCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230
Db 1141 TTTTCTAAAGCTCCCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1200
QY 1231 GGCTTTCATGGGAATGATGAAGATGATAAGTGAAGAAATGTTATCATTTATCATGAAG 1290
Db 1201 GGCTTTCATGGGAATGATGAAGATGATAAGTGAAGAAATGTTATCATTTATCATGAAG 1260
QY 1291 TACCATATCATATACATGAACCTTTATTTATTTGCTTACCATCATCTTGGGCTGAAT 1350
Db 1261 TACCATATCATATACATGAACCTTTATTTATTTGCTTACCATCATCTTGGGCTGAAT 1320
QY 1351 AATGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGACCTGTACCTTCTGTG 1410
Db 1321 AATGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGACCTGTACCTTCTGTG 1380
QY 1411 GCAGAAAGGACAGTGAGATGATTAAGTTAAGGACTTTGAGATGAGAGGTTATCT 1470
Db 1381 GCAGAAAGGACAGTGAGATGATTAAGTTAAGGACTTTGAGATGAGAGGTTATCT 1440
QY 1471 TGCTGATTGAGTGGGCCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGAA 1530

Db 1441 TGCTGATTGAGTGGGCCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGAA 1500
QY 1531 GGTCAAAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGTGTGACCTGAGCAGGG 1590
Db 1501 GGTCAAAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGTGTGACCTGAGCAGGG 1560
QY 1591 GCATGATGTCGCGAGCCTTTCAGATGCCAGAAAGGAAAGAAATGATTCCTTSCCTGG 1650
Db 1561 GCATGATGTCGCGAGCCTTTCAGATGCCAGAAAGGAAAGAAATGATTCCTTSCCTGG 1620
QY 1651 AGCTTCCAAAAGAAACACAGCCCTGCCACGCTTTCACCTTGAGCCCATTTGAAACTGATCTT 1710
Db 1621 AGCTTCCAAAAGAAACACAGCCCTGCCACGCTTTCACCTTGAGCCCATTTGAAACTGATCTT 1680
QY 1711 GAGCTCTTGGCTTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAAGAAAAAAA 1770
Db 1681 GAGCTCTTGGCTTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAAGAAAAAAA 1740
QY 1771 AAAAAAAGAAAAAAA 1786
Db 1741 AAAAAAAGAAAAAAA 1756

RESULT 4

ACD68612

ID ACD68612 standard; cDNA; 1837 BP.

XX ACD68612;

XX ACD68612;

DT 17-SEP-2003 (first entry)

XX

XX Novel human secreted and transmembrane protein PRO10111 cDNA.

XX

XX Human; secreted and transmembrane protein; PRO; cytostatic;

KW antarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

KW pharmacological; diagnostic; biosensor; bioreactor; tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW liver tumour; bone disorder; cartilage disorder; sports injury;

KW arthritis; wound; gene; ss.

XX

XX Homo sapiens.

XX

XX US2003045687-A1.

XX

XX 06-MAR-2003.

XX

XX 12-AUG-2002; 2002US-00218631.

PF

XX 01-JUN-2001; 2001WO-US017800.

PR

XX 29-JUN-2001; 2001WO-US021066.

PR

XX 09-APR-2002; 2002US-00119480.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX

XX WPI: 2003-512315/48.

XX

XX P-PSDB; AB033724.

DR

XX Claim 2; Fig 39; 314pp; English.

PS

XX The invention describes an isolated nucleic acid molecule comprising a

CC sequence with at least 80% identity to: (a) a nucleotide encoding or

CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are

CC fully defined in the specification; or (b) any of 122 nucleotide

CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ

Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 7; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY	32	ACCACGAGGCTGGGAGTCTAGTTTGTCTGCTGCGCAGGCTCCACTGAGGGGAAAC	91
DB	1	ACCACGAGGCTGGGAGTCTAGTTTGTCTGCTGCGCAGGCTCCACTGAGGGGAAAC	60
QY	92	GGGAGCCTGTCTGAGAGAAAGATGCCCTGCTGTGACACTCTACTGCTCTCTCTTGGCTC	151
DB	61	GGGAGCCTGTCTGAGAGAAAGATGCCCTGCTGTGACACTCTACTGCTCTCTCTTGGCTC	120
QY	152	TCAGCTACTCGATTGCCACTCAATACACCGGTCCACAAACAGTGAATGGTTGGAGCGG	211
DB	121	TCAGCTACTCGATTGCCACTCAATACACCGGTCCACAAACAGTGAATGGTTGGAGCGG	180
QY	212	GGCTCTTGACCGTGCAGTGTGTACAGATCAGCTGGGAGACTTCTGAAGTGGTGG	271
DB	181	GGCTCTTGACCGTGCAGTGTGTACAGATCAGCTGGGAGACTTCTGAAGTGGTGG	240
QY	272	TGTCAGAGGATTTTGGGTGACTGCAAGATTCCTTGTGTTAAACACAGTGGTTCAGAGAG	331
DB	241	TGTCAGAGGATTTTGGGTGACTGCAAGATTCCTTGTGTTAAACACAGTGGTTCAGAGAG	300
QY	332	GAGGTGAAGAGGACCGGGTGTCCATCAAGACCAATCAGAAAAACCGCAGTTCACCTGTG	391
DB	301	GAGGTGAAGAGGACCGGGTGTCCATCAAGACCAATCAGAAAAACCGCAGTTCACCTGTG	360
QY	392	ACCATGAGGATCTCATGAAACCTGATCTGACACTTACTGGTGGAAATGAGAAAACT	451
DB	361	ACCATGAGGATCTCATGAAACCTGATCTGACACTTACTGGTGGAAATGAGAAAACT	420
QY	452	GGAAATGACCTTGGGTGACAGTTCAGTGAACCTGACCCAGCAGCAGTCAACCCAGAA	511
DB	421	GGAAATGACCTTGGGTGACAGTTCAGTGAACCTGACCCAGCAGCAGTCAACCCAGAA	480
QY	512	GAAACTAGCAGTCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGCACAAGCTCCTG	571
DB	481	GAAACTAGCAGTCTCCCAACTCTGACCGGCCACCACTTGGACAAACAGGCACAAGCTCCTG	540
QY	572	AAGCTCAGTGTCTCTGCGCTCATCTTACCATATATKYTGCTTTTGGTGGCCGCC	631
DB	541	AAGCTCAGTGTCTCTGCGCTCATCTTACCATATATKYTGCTTTTGGTGGCCGCC	600
QY	632	TCACCTTTGGCTTGAGAGATGATGAAGTACCAGCAGAAAGACGCGGGATGTCCTCCAGAG	691
DB	601	TCACCTTTGGCTTGAGAGATGATGAAGTACCAGCAGAAAGACGCGGGATGTCCTCCAGAG	660
QY	692	CAGGTACTGCGCCCTGGAGGGCGACCTCTGCTATGACAGACCTGACCCCTGACCTGGCC	751

DB	661	CAGGTACTGCGCCCTGGAGGGCGACCTCTGCTATGACAGCTGACCTGCGCTGGCC	720
QY	752	GGAACCTCCCGCGAAAGGCTACCAAGAGCTTTCTCTGCGCCAGGTTGACAGGTGAA	811
DB	721	GGAACCTCCCGCGAAAGGCTACCAAGAGCTTTCTCTGCGCCAGGTTGACAGGTGAA	780
QY	812	GTGGATATGTCAACATGCTTCTTCCGAGAGGACATTTCTATGCTCTCTGACC	871
DB	781	GTGGATATGTCAACATGCTTCTTCCGAGAGGACATTTCTATGCTCTCTGACC	840
QY	872	TTGGGTGTGAGGATCAGGAACCGACCTACTCTCAACATGGGCCNMCTCAGTAGCCAMCTY	931
DB	841	TTGGGTGTGAGGATCAGGAACCGACCTACTCTCAACATGGGCCNMCTCAGTAGCCAMCTY	900
QY	932	CCCGGAGGGGCGCTGAGGAGCCACGGAATACAGACATCAGCAGCCCTTAGCCTGCA	991
DB	901	CCCGGAGGGGCGCTGAGGAGCCACGGAATACAGACATCAGCAGCCCTTAGCCTGCA	960
QY	992	CTCCAGGCTCTCTTCTTGGACCCCGAGGCTGTGAGACACTCTCTGCGCTCATCGACCGTCTGC	1051
DB	961	CTCCAGGCTCTCTTCTTGGACCCCGAGGCTGTGAGACACTCTCTGCGCTCATCGACCGTCTGC	1020
QY	1052	CCCTGCTCCCTCATCAGGACCAACCGGGGACTGGTGCCTCTGCTGATCAGCAGCA	1111
DB	1021	CCCTGCTCCCTCATCAGGACCAACCGGGGACTGGTGCCTCTGCTGATCAGCAGCA	1080
QY	1112	TTGCCCCCTAGCTCTGGTTGGGCTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTTGGGG	1171
DB	1081	TTGCCCCCTAGCTCTGGTTGGGCTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTTGGGG	1140
QY	1172	TTTTCTAAACGTCCTCTCTCT-CTACATAGTTGAGAGGGGGCTAGGGAATGCTCTGG	1230
DB	1141	TTTTCTAAACGTCCTCTCTCTCTACATAGTTGAGAGGGGGCTAGGGAATGCTCTGG	1200
QY	1231	GGCTTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1290
DB	1201	GGCTTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1260
QY	1291	TACCATTTATCATTAATACAAATGAACCTTTATTTATTCCTTACACATGTTATGGGTGAAT	1350
DB	1261	TACCATTTATCATTAATACAAATGAACCTTTATTTATTTGCTTACCACATGTTATGGGTGAAT	1320
QY	1351	AATGGCCCCCAAGATATCTGTCTCTAATCTCTCAGAACTTGTGACTGTTACTTCTGTG	1410
DB	1321	AATGGCCCCCAAGATATCTGTCTCTAATCTCTCAGAACTTGTGACTGTTACTTCTGTG	1380
QY	1411	GCAGAAAGGACAGTCAGATGATGTAAGTTTAAGGACTTTTGAGATAGAGAGTTTATCT	1470
DB	1381	GCAGAAAGGACAGTCAGATGATGTAAGTTTAAGGACTTTTGAGATAGAGAGTTTATCT	1440
QY	1471	TGCTGATTCAGTGGGCCCCAAAATATACCAAGGGTCTCTCATAGAAAGAGGCGCAGAA	1530
DB	1441	TGCTGATTCAGTGGGCCCCAAAATATACCAAGGGTCTCTCATAGAAAGAGGCGCAGAA	1500
QY	1531	GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTGGAGCTGGGTGTGACCTGAGCAGGG	1590
DB	1501	GGTCAAGAGGTAGAGACAAAGTGTATGTAAGTGGAGCTGGGTGTGACCTGAGCAGGG	1560
QY	1591	GCATGAATGCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTTCCTCTGG	1650
DB	1561	GCATGAATGCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTTCCTCTGG	1620
QY	1651	AGCTTCCAAAAGAAACCGACCTGCCCGCTTCACTTTGAGCCCATTTGAAACTGATCTT	1710
DB	1621	AGCTTCCAAAAGAAACCGACCTGCCCGCTTCACTTTGAGCCCATTTGAAACTGATCTT	1680
QY	1711	GAGCTCTCTGGCTCCAGAAATTCAGAGGAATAAATTTGTGTTTAAATGAAAAAAA	1770
DB	1681	GAGCTCTCTGGCTCCAGAAATTCAGAGGAATAAATTTGTGTTTAAATGAAAAAAA	1740
QY	1771	AAAAAAGAAAAA	1786

	Db	1741 AAAAAAAAAAAAAA 1756	
		RESULT 5	
		ACA68516	
	ID	ACA68516 standard; cDNA; 1837 BP.	
	XX	AC	
	XX	AC	
	XX	DT	
	XX	(first entry)	
	DE	25-JUN-2003	
	XX	Novel human secreted and transmembrane protein PRO10111 cDNA.	
	XX	Human; secreted and transmembrane protein; PRO; cardiac; cytostatic;	
	KW	antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;	
	KW	gene therapy; cardiovascular disorder; endothelial disorder;	
	KW	angiogenic disorder; cardiac hypertrophy; trauma; cancer;	
	KW	age-related macular degeneration; atherosclerosis; hypertension;	
	KW	arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;	
	KW	thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;	
	KW	liver carcinoma; wound healing; chromosome mapping; gene mapping; Gene;	
	ss.		
	OS	Homo sapiens.	
	XX	US2003088063-A1.	
	PV	08-MAY-2003.	
	PF	12-AUG-2002; 2002US-00219003.	
	XX	25-JUL-2000; 2000US-0220664P.	
	PR	01-JUN-2001; 2001WO-US017800.	
	PR	29-JUN-2001; 2001WO-US021086.	
	PR	09-APR-2002; 2002US-00119480.	
	XX	(GETH) GENENTECH INC.	
	XX	Baker KP, Deancovers L, Gerritsen WE, Goddard A, Godowski PJ;	
	PI	Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;	
	PI	P-PDB; ABUS2067.	
	XX	WPI; 2003-393229/37.	
	DR	One hundred and eighty seven nucleic acids encoding PRO polypeptides,	
	DR	useful in diagnosis and treatment of cardiovascular (e.g. myocardial	
	PT	infarction), endothelial or angiogenic disorders in a mammal.	
	PT	Claim 2; Fig 39; 314pp; English.	
	PS	The invention describes one hundred and eighty seven nucleic acids	
	XX	encoding novel human secreted and transmembrane (PRO) polypeptides. The	
	CC	PRO nucleic acids, polypeptides, agonists and antagonists are useful for	
	CC	treating or diagnosing a cardiovascular, endothelial or angiogenic	
	CC	disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-	
	CC	related macular degeneration, atherosclerosis, hypertension, arterial	
	CC	restenosis, rheumatoid arthritis, angina, myocardial infarctions,	
	CC	thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast	
	CC	carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids	
	CC	have applications in molecular biology, including use as hybridisation	
	CC	probes, and in chromosome and gene mapping. This sequence encodes a novel	
	CC	human secreted and transmembrane PRO polypeptide	
	XX	Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;	
	SQ	Query Watch 97.0%; Score 1741.6; DB 7; Length 1837;	
		Best Local Similarity 99.6%; Pred. No. 0;	
		Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;	
	QY	32 ACCAGCAGAAGCGTGGAGTCGTAGTTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 91	
	Df	1 ACCAGCAGAAGCGTGGAGTCGTAGTTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 60	

Db 1141 TTTTCTAAACGTCCTCTCTCCCTACATGATGTTGAGGAGGGCTAGGGATATGCTCTGG 1200
 Qy 1231 GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATTATCATGAAG 1290
 Db 1201 GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATTATCATGAAG 1260
 Qy 1291 TACCAATTATCAATAACATGAACCTTTATTTATTTGCTCCATCCACATGTTATGGGCTGAAT 1350
 Db 1261 TACCAATTATCAATAACATGAACCTTTATTTATTTGCTCCATCCACATGTTATGGGCTGAAT 1320
 Qy 1351 AATGGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTCTTACCTTCTGTG 1410
 Db 1321 AATGGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTCTTACCTTCTGTG 1380
 Qy 1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGAGTTATTCT 1470
 Db 1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGAGTTATTCT 1440
 Qy 1471 TGCTGATTCAGGTGGGCCCCAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA 1530
 Db 1441 TGCTGATTCAGGTGGGCCCCAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA 1500
 Qy 1531 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTGACCTGAGCAGGG 1590
 Db 1501 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTGACCTGAGCAGGG 1560
 Qy 1591 GCATGATGTCGCGAGCTTCCAGATGCCAGAAAGGAAGGAATGGAATCCCTGCTCTGG 1650
 Db 1561 GCATGATGTCGCGAGCTTCCAGATGCCAGAAAGGAAGGAATGGAATCCCTGCTCTGG 1620
 Qy 1651 AGCTCCAAAAGAAACCCAGCCCTGCCACGCTTGACCTTGAGCCCATTTGAAACTGATCTT 1710
 Db 1621 AGCTCCAAAAGAAACCCAGCCCTGCCACGCTTGACCTTGAGCCCATTTGAAACTGATCTT 1680
 Qy 1711 GAGCTCTGGCTCCAGAAATGTCAGAGAAATAAATTTGTTGTTTAAATGAAAAAAA 1770
 Db 1681 GAGCTCTGGCTCCAGAAATGTCAGAGAAATAAATTTGTTGTTTAAATGAAAAAAA 1740
 Qy 1771 AAAAAAAAAAAAAA 1786
 Db 1741 AAAAAAAAAAAAAA 1756
 RESULT 6
 ID ABT44245
 XX ABT44245 standard; cDNA; 1837 BP.
 AC ABT44245;
 XX
 DT 06-NOV-2003 (first entry)
 DE Human PRO10111 cDNA.
 XX
 KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss;
 KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
 KW cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003050448-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002US-00230414.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR WPI; 2003-521818/49.
 DR P-PSDB; ABJ72247.
 XX
 PT New nucleic acid encoding for a PRO protein, useful for the manufacture
 of a medicament for diagnosing or treating tumors or for measuring or
 detecting expression of an associated gene.
 PT
 XX Claim 2; Fig 39; 315pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid encoding a fully
 defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of INF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell
 CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC cDNA of the invention
 CC
 SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
 Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 Qy 32 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTCTGCTGCCAGGTCCACTGAGGGGAAAC 91
 Db 1 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTCTGCTGCCAGGTCCACTGAGGGGAAAC 60
 Qy 92 GGGGACCTCTCTGAGAGAGAGATGCCCTGCTGACACTTACTCTCTCTCTCTCTGGCTC 151
 Db 61 GGGGACCTCTCTGAGAGAGAGATGCCCTGCTGACACTTACTCTCTCTCTCTCTGGCTC 120
 Qy 152 TCAGGCTACTCTCAATGCCACTCAAAATCACCGGTCCAAACAGTGAATGGCTTGGAGGG 211
 Db 121 TCAGGCTACTCTCAATGCCACTCAAAATCACCGGTCCAAACAGTGAATGGCTTGGAGGG 180
 Qy 212 GGCTCTCTGACCGTGCAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
 Db 181 GGCTCTCTGACCGTGCAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240
 Qy 272 TGTGAGGAGCTATTTGGGCTGACTGCAAGATCTTGTAAACCCAGTGGGTTCAGAGCAG 331
 Db 241 TGTGAGGAGCTATTTGGGCTGACTGCAAGATCTTGTAAACCCAGTGGGTTCAGAGCAG 300
 Qy 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGCAATCAAGAAACCCGACGTTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGCAATCAAGAAACCCGACGTTTCACTGTG 360
 Qy 392 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGTGTGGAAATTCAGAAAACT 451
 Db 361 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGTGTGGAAATTCAGAAAACT 420
 Qy 452 GGAATAGACCTTTGGGCTCACAGTTCAAGTGACCAATGACCCAGCACCAGTCAACCAAGAA 511
 Db 421 GGAATAGACCTTTGGGCTCACAGTTCAAGTGACCAATGACCCAGCACCAGTCAACCAAGAA 480
 Qy 512 GAAACTAGCAGCTCCCCCACTCTGACCGGCACTTTGGCAACAGGACAGTCTCTG 571
 Db 481 GAAACTAGCAGCTCCCCCACTCTGACCGGCACTTTGGCAACAGGACAGTCTCTG 540
 Qy 572 AAGCTCAGTGTCTCTCTGCTCCCTCATCTTACCATATTTKTYGTCTTTTGGTGGCCGCC 631
 Db 541 AAGCTCAGTGTCTCTCTGCTCCCTCATCTTACCATATTTGCTGCTCTTTTGGTGGCCGCC 600
 Qy 632 TCACCTCTTGGCTTGGAGGATGATGAAGTACAGGAGAAAGCAGCGGATGTCTCCACAG 691
 Db 601 TCACCTCTTGGCTTGGAGGATGATGAAGTACAGGAGAAAGCAGCGGATGTCTCCACAG 660

QY 212 GGCTCCTTACCGTGCAGTGTGTTTACAGATCAGCTGGAGACCTACTTGAAGTGGTG 271
 Db 181 GGCTCCTTGAACGTCAGTGTGTTTACAGATCAGCTGGAGACCTACTTGAAGTGGTG 240
 QY 272 TGTGAGGAGCTATTGCGGTGACTGCAAGATCCCTTGTGTTAAACCAAGTGGGTGAGAG 331
 Db 241 TGTGAGGAGCTATTGCGGTGACTGCAAGATCCCTTGTGTTAAACCAAGTGGGTGAGAG 300
 QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGCACGTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGCACGTTCACTGTG 360
 QY 392 ACCATGGAGATCTCATGAAAACTGATGTGACACTTACTGTTGGAATTTGAAAACT 451
 Db 361 ACCATGGAGATCTCATGAAAACTGATGTGACACTTACTGTTGGAATTTGAAAACT 420
 QY 452 GGAATGACCTTGGGTGACAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 511
 Db 421 GGAATGACCTTGGGTGACAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 480
 QY 512 GAACTAGCAGCTCCCACTCTGACCGGCCACCACTTTGACACAGGACCAAGCTCTCTG 571
 Db 481 GAACTAGCAGCTCCCACTCTGACCGGCCACCACTTTGACACAGGACCAAGCTCTCTG 540
 QY 572 AGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
 Db 541 AGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 632 TCACCTCTTGGCTTGGAGTATGATGAAGTACACAGAGAACGAGCGGGATGTCCTCCAGAG 691
 Db 601 TCACCTCTTGGCTTGGAGTATGATGAAGTACACAGAGAACGAGCGGGATGTCCTCCAGAG 660
 QY 692 CAGGTACTGACCCCTGAGGGGAGCTCTGCTATGACAGACCTGACCTGACCTGAGCTGCC 751
 Db 661 CAGGTACTGACCCCTGAGGGGAGCTCTGCTATGACAGACCTGACCTGAGCTGCC 720
 QY 752 GGAACCTCCCGGAAAGGCTACACAGAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
 Db 721 GGAACCTCCCGGAAAGGCTACACAGAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 812 GTGGAATATGACCATGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
 Db 781 GTGGAATATGACCATGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 872 TTGGTGTCTGAGGATCAGGACCCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
 Db 841 TTGGTGTCTGAGGATCAGGACCCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 932 CCGGACAGGGCCCTGAGGAGCCCAAGGATACAGCACCACATCAGCAGCCCTTAGCCTGCA 991
 Db 901 CCGGACAGGGCCCTGAGGAGCCCAAGGATACAGCACCACATCAGCAGCCCTTAGCCTGCA 960
 QY 992 CTCAGGCTCTCTTGTGACCCGAGGCTGTGAGCAGACCTCTGCTGCTGCTGCTGCTGCTG 1051
 Db 961 CTCAGGCTCTCTTGTGACCCGAGGCTGTGAGCAGACCTCTGCTGCTGCTGCTGCTGCTG 1020
 QY 1052 CCCCTGCTCCCTCTCATCAGGACCAACCCGGGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
 Db 1021 CCCCTGCTCCCTCTCATCAGGACCAACCCGGGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 QY 1112 TTGCCCTAGCTCTGGGTGCTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1171
 Db 1081 TTGCCCTAGCTCTGGGTGCTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1140
 QY 1172 TTTTCTAAACCTCCCTCTCTCTCATAGTTCAGGAGGGGCTAGGGATATGCTCTGG 1230
 Db 1141 TTTTCTAAACCTCCCTCTCTCTCATAGTTCAGGAGGGGCTAGGGATATGCTCTGG 1200
 QY 1231 GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATCATGAAG 1290
 Db 1201 GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATTTATCATGAAG 1260

QY 1291 TACCATTATCATATCAATGAACCTTTATTTATTCCTTACCATCATGTTTATGGCTGAAT 1350
 Db 1261 TACCATTATCATATCAATGAACCTTTATTTATTCCTTACCATCATGTTTATGGCTGAAT 1320
 QY 1351 AATGGCCCCCAAGATATCTGTGTCTCTAATCTCTCAGAACTTGTGACTGTACTCTGTG 1410
 Db 1321 AATGGCCCCCAAGATATCTGTGTCTCTAATCTCTCAGAACTTGTGACTGTACTCTGTG 1380
 QY 1411 GCAGAAAGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATAGAGAGGTTATCT 1470
 Db 1381 GCAGAAAGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATAGAGAGGTTATCT 1440
 QY 1471 TGCTGATTCAAGTGGGCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGAA 1530
 Db 1441 TGCTGATTCAAGTGGGCCCAAAATATCACCAAGGGTCTCTCATAGAAAGAGGCCAGAA 1500
 QY 1531 GGTCAAGAGGTAGACAAAGTGTATGTAAAGTTAAGGACTTTGAGAGTGCAGTGCAGGG 1590
 Db 1501 GGTCAAGAGGTAGACAAAGTGTATGTAAAGTTAAGGACTTTGAGAGTGCAGTGCAGGG 1560
 QY 1591 GCCATGAATCCCGCAGCCTTCAGATGCCAGAAAGGAAAGGAATGATTCCTCCCTGCTGG 1650
 Db 1561 GCCATGAATCCCGCAGCCTTCAGATGCCAGAAAGGAAAGGAATGATTCCTCCCTGCTGG 1620
 QY 1651 AGCTCTCAAGAAAGAACCCAGCCTTCCAGCCCTTCCAGCTTGCCTTGCCTTGCCTGCT 1710
 Db 1621 AGCTCTCAAGAAAGAACCCAGCCTTCCAGCCCTTCCAGCTTGCCTTGCCTTGCCTGCT 1680
 QY 1711 GAGCTCTGCTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAATGAAAAAAA 1770
 Db 1681 GAGCTCTGCTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAATGAAAAAAA 1740
 QY 1771 AAAAAAAGAAAAA 1786
 Db 1741 AAAAAAAGAAAAA 1756

RESULT 8

ACD82195
ID ACD82195 standard; cDNA; 1837 BP.

XX ACD82195;

XX AC

XX DT 19-SEP-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO 10111 cDNA.

DE Human; ss; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;

KW human dermal fibroblast stimulation; tumour; tissue typing; gene;

KW affinity purification.

XX Homo sapiens.

XX US2003044934-A1.

XX 06-MAR-2003.

XX 28-AUG-2002; 2002US-00230338.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Deansoyers L, Gerritsen ME, Goddard A, Godowski PJ,

PI Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;

XX WPI; 2003-492274/46.

XX P-PSDB; ABO34270.

PT New transmembrane polypeptides and nucleic acids encoding the

PT polypeptides, useful in gene therapy, in chromosome identification, as

QY	152	TCAGGCTACTCATTTGCCACTCAAAATCAACCGGTCCAAACACAGTGAATGGCTTGGAGCGG	211
DB	121	TCAGGCTACTCATTTGCCACTCAAAATCAACCGGTCCAAACACAGTGAATGGCTTGGAGCGG	180
QY	212	GGCTCCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGTGG	271
DB	181	GGCTCCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGTGG	240
QY	272	TGTCGAGGAGCTATTTTGGGTGCACTGCAAGATCCCTTTGTTAAAAACAGTGGGTCAAGCAG	331
DB	241	TGTCGAGGAGCTATTTTGGGTGCACTGCAAGATCCCTTTGTTAAAAACAGTGGGTCAAGCAG	300
QY	332	GAGGTGAAGAGGGACCGGGTGCATCAAGGACACATCAGAANAACCGCACGCTTCACTGTG	391
DB	301	GAGGTGAAGAGGGACCGGGTGCATCAAGGACACATCAGAANAACCGCACGCTTCACTGTG	360
QY	392	ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGGTGTGGAAATTCAGAAAACT	451
DB	361	ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGGTGTGGAAATTCAGAAAACT	420
QY	452	GGAAATGACCTTGGGGTCAAGTTCAGATGACCATTTGACCCAGCACCAAGTCAACCAAGAA	511
DB	421	GGAAATGACCTTGGGGTCAAGTTCAGATGACCATTTGACCCAGCACCAAGTCAACCAAGAA	480
QY	512	GAAACTAGCAGCTCCCCAACTCTGACCGGCCACACATTGGACAACAGGCACAAGCTCCTG	571
DB	481	GAAACTAGCAGCTCCCCAACTCTGACCGGCCACACATTGGACAACAGGCACAAGCTCCTG	540
QY	572	AAGCTCAGTGTCTCTGCCCTCATCTTCAACATATTKYTYGTCCTTTGGTGGCGGCC	631
DB	541	AAGCTCAGTGTCTCTGCCCTCATCTTCAACATATTTGCTGTGCTTTTGGTGGCGGCC	600
QY	632	TCACCTTTGGCTTGGAGGATCATGAAGTACCAGCAGAAAGCAGCGGGATGTCCCCAGAG	691
DB	601	TCACCTTTGGCTTGGAGGATCATGAAGTACCAGCAGAAAGCAGCGGGATGTCCCCAGAG	660
QY	692	CAGGTACTGACGCCCTGGAGGGCGACCTCTGTATGCAGACCTGACCCCTGCAGCTGGCC	751
DB	661	CAGGTACTGACGCCCTGGAGGGCGACCTCTGTATGCAGACCTGACCCCTGCAGCTGGCC	720
QY	752	GGAACTCCCGCGAAAGGCTACACGAAGCTTTCTCTGCGCCAGGTTGACCAGGTGAA	811
DB	721	GGAACTCCCGCGAAAGGCTACACGAAGCTTTCTCTGCGCCAGGTTGACCAGGTGAA	780
QY	812	GTGGAATATGTCAACATGGCTTCCTTGCAGGAGGAGACATTTCCCTATGCATCTCTGACC	871
DB	781	GTGGAATATGTCAACATGGCTTCCTTGCAGGAGGAGACATTTCCCTATGCATCTCTGACC	840
QY	872	TTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCCACMCTCAGTAGGCCMCTY	931
DB	841	TTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCCACMCTCAGTAGGCCMCTC	900
QY	932	CCGGCAGGGGCCCTTGAGGAGCCACCGAATACAGCACCATCAGCAGGCTTACGCTGTCA	991
DB	901	CCGGCAGGGGCCCTTGAGGAGCCACCGAATACAGCACCATCAGCAGGCTTACGCTGTCA	960
QY	992	CTCAGGCTCTTCTTGGACCCGAGGTGTAGCACACTCTGTGCTCATCGACCGTCTGC	1051
DB	961	CTCAGGCTCTTCTTGGACCCGAGGTGTAGCACACTCTGTGCTCATCGACCGTCTGC	1020
QY	1052	CCCTGTCTCCCTCATCAGACCAACCCGGGACTGTGTGCTCTGTGCTGATCAGCCAGCA	1111
DB	1021	CCCTGTCTCCCTCATCAGACCAACCCGGGACTGTGTGCTCTGTGCTGATCAGCCAGCA	1080
QY	1112	TTGCCCCTAGCTCTGGCTTGGGTCAGGTCCTCAGGGGCTTCTAGGAGTTGGGG	1171
DB	1081	TTGCCCCTAGCTCTGGCTTGGGTCAGGTCCTCAGGGGCTTCTAGGAGTTGGGG	1140
QY	1172	TTTTCCTAAAGGTCCTCTCTCTCTCATATAGTTGAGGAGGGGCTAGGATATGCTCTG	1230
DB	1141	TTTTCCTAAAGGTCCTCTCTCTCTCATATAGTTGAGGAGGGGCTAGGATATGCTCTG	1200
QY	1231	GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTATATCATTTATATCATGAAG	1290

Db	1201	GGCTTTTCATGGGAATGATGAAGATGATATGAGAAAATGTTATCATTTATTATTCATGAAG	1260
Qy	1291	TACCAATTATCATAAATACAAATGAACCTTTATTTATTCGCTACCAATGTTATGGCTGGAAT	1350
Db	1261	TACCAATTATCATAAATACAAATGAACCTTTATTTATTCGCTACCAATGTTATGGCTGGAAT	1320
Qy	1351	AATGGCCCCAAAGATATCTGTCTCTTAATCTTCAGAACTTGTGACTGTTCCTTCTGTG	1410
Db	1321	AATGGCCCCAAAGATATCTGTCTCTTAATCTTCAGAACTTGTGACTGTTCCTTCTGTG	1380
Qy	1411	GCAGAAAGGACACAGTCAGATGTATGTAAAGTAAAGACATTTGAGATAGAGAGTTATCT	1470
Db	1381	GCAGAAAGGACACAGTCAGATGTATGTAAAGTAAAGACATTTGAGATAGAGAGTTATCT	1440
Qy	1471	TGCTGATTTCAGGTGGGCCCAAAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA	1530
Db	1441	TGCTGATTTCAGGTGGGCCCAAAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA	1500
Qy	1531	GGTCAAGAGGTATAGACAAAGTGATGGAGTGGACGTGGGTGTGACGTGAGCAGGG	1590
Db	1501	GGTCAAGAGGTATAGACAAAGTGATGGAGTGGACGTGGGTGTGACGTGAGCAGGG	1560
Qy	1591	GCCATGAATGCCCGACGCTTCAGATGCCAGAAAGGAAAAGGAATGGATTCCTCTGCTGG	1650
Db	1561	GCCATGAATGCCCGACGCTTCAGATGCCAGAAAGGAAAAGGAATGGATTCCTCTGCTGG	1620
Qy	1651	AGCCTCAAAAGAAACAGCCCTGCCACGCCTTGACTTGAGCCCAATGAAAATGATCTT	1710
Db	1621	AGCCTCAAAAGAAACAGCCCTGCCACGCCTTGACTTGAGCCCAATGAAAATGATCTT	1680
Qy	1711	GAGCTCTGGCCTCCAGAAATTCGAGAGAAATAAATTTGTTGTTTTTAATGAAAAAAA	1770
Db	1681	GAGCTCTGGCCTCCAGAAATTCGAGAGAAATAAATTTGTTGTTTTTAATGAAAAAAA	1740
Qy	1771	AAAAAAAAAAAAAAAAAAAA	1786
Db	1741	AAAAAAAAAAAAAAAAAAAA	1756

RESULT 11
ADB80635

AD80635
ID AD80635 standard: cDNA: 1837 BP.

AC ADB80635;

DT 04-DEC-2003 (first entry)

XX
DE Novel human secreted and transmembrane protein PRO10111 cDNA

Human; secreted and transmembrane protein; PRO; gene; ss; cyostatic; vulvarey; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

XX Homo sapiens.

XX
PN
US2003088068-A1.XX
PD 08-MAY-2003.

XX
PF 13-AUG-2002: 2002US-00219481.

XX
PR 01-JUN-2001: 2001WO-US017800

PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480

XX
DA (GETH) GENENTECH INC

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-657982/62.
XX P-PSDB; ADB0636.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX Claim 2; Fig 39; 305pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (i). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO1275, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO331, PRO723, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
CC PRO3940, PRO5079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (i) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (ii) encoding (i) is
CC useful for chromosome and gene mapping or gene therapy. (ii) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This sequence encodes a human secreted and transmembrane
CC PRO polypeptide.
XX
XX Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAGCGCTGGAGTCTGTAGTTTGTCTCTGTCGCCAGGCTCCAGCTGAGGGGAAC 91
DB 1 ACCAGCAGAGCGCTGGAGTCTGTAGTTTGTCTCTGTCGCCAGGCTCCAGCTGAGGGGAAC 60
QY 92 GGGGACCTGCTGGAAGAGAAGATGCCCTGTGACACTCTACCTGCTCTCTCTTCTGGCTC 151
DB 61 GGGGACCTGCTGGAAGAGAAGATGCCCTGTGACACTCTACCTGCTCTCTCTTCTGGCTC 120
QY 152 TCAGGCTACTCCATTGCCACTCAATACACCGGTCCAAACAAAGTGAATGGTGTGGAGCGG 211
DB 121 TCAGGCTACTCCATTGCCACTCAATACACCGGTCCAAACAAAGTGAATGGTGTGGAGCGG 180
QY 212 GGCCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTTACTTGAAGTGTGG 271
DB 181 GGCCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACTTACTTGAAGTGTGG 240
QY 272 TGTGAGGAGCTATTGTGGCGTGACTGCAAGATCTTGTGTTAAACACAGTGGGTCCAGAGCAG 331
DB 272 TGTGAGGAGCTATTGTGGCGTGACTGCAAGATCTTGTGTTAAACACAGTGGGTCCAGAGCAG 331
DB 241 TGTGAGGAGCTATTGTGGCGTGACTGCAAGATCTTGTGTTAAACACAGTGGGTCCAGAGCAG 300
QY 332 GAGGTGAAGAGGAGCCGGGTGTCTCATCAAGACAAATCAGAAAAACCGACCTTCTACTGTG 391
DB 301 GAGGTGAAGAGGAGCCGGGTGTCTCATCAAGACAAATCAGAAAAACCGACCTTCTACTGTG 360
QY 392 ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGTGTGGAATTCAGAAAAACT 451
DB 361 ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGTGTGGAATTCAGAAAAACT 420
QY 452 GGAATGACCTTTGGGTCACAGTTCACAGTTCACAGTTCACAGTTCACAGTTCACAGTTCAC 511
DB 421 GGAATGACCTTTGGGTCACAGTTCACAGTTCACAGTTCACAGTTCACAGTTCACAGTTCAC 480
QY 512 GAACTAGCAGTCCCGCACTCTGACCGGCCCACTTTGGACAAACAGGCAACAAGTCTCTG 571
DB 481 GAACTAGCAGTCCCGCACTCTGACCGGCCCACTTTGGACAAACAGGCAACAAGTCTCTG 540
QY 572 AAGCTCAGTGTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 631
DB 541 AAGCTCAGTGTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
QY 632 TCACCTTTGGCTTTGGAGGATGATGAAGTACACAGCAGAAAGCAGCGGGATGTCCTCCAGAG 691
DB 601 TCACCTTTGGCTTTGGAGGATGATGAAGTACACAGCAGAAAGCAGCGGGATGTCCTCCAGAG 660
QY 692 CAGGTACTGCAGCCCTTGAGGCGGCACTCTGCTATGACAGACCTGACCTCTGAGTGGCC 751
DB 661 CAGGTACTGCAGCCCTTGAGGCGGCACTCTGCTATGACAGACCTGACCTCTGAGTGGCC 720
QY 752 GGAACCTCCCGGAAAGGCTACCAAGCTTTCTCTGCTGCCAGGTTGACAGGTGAA 811
DB 721 GGAACCTCCCGGAAAGGCTACCAAGCTTTCTCTGCTGCCAGGTTGACAGGTGAA 780
QY 812 GTGGATATGTACCATGCTTCTTGGCGAAGGAGGACATTTCTATGCACTCTGACC 871
DB 781 GTGGATATGTACCATGCTTCTTGGCGAAGGAGGACATTTCTATGCACTCTGACC 840
QY 872 TTGGGTGTGAGGATCAGGAACCGACCTACTGCAACATGGGCGGCACTCAGTAGCCAMCTY 931
DB 841 TTGGGTGTGAGGATCAGGAACCGACCTACTGCAACATGGGCGGCACTCAGTAGCCAMCTY 900
QY 932 CCGGCGAGGGGCTGAGGAGCCGAGGATACACCAATCAGCAGGCTTAGGCTGCA 991
DB 901 CCGGCGAGGGGCTGAGGAGCCGAGGATACACCAATCAGCAGGCTTAGGCTGCA 960
QY 992 CTCAGGCTCCTTCTTGGACCCCGAGGCTGTGAGCAGACTCTCTGCTCATFCGACCGTCTGC 1051
DB 961 CTCAGGCTCCTTCTTGGACCCCGAGGCTGTGAGCAGACTCTCTGCTCATFCGACCGTCTGC 1020
QY 1052 CCGCTGCTCCCTCATCAGGACCAACCCCGGAGCTGGTGCCTCTGCTCATCAGCCAGCA 1111
DB 1021 CCGCTGCTCCCTCATCAGGACCAACCCCGGAGCTGGTGCCTCTGCTCATCAGCCAGCA 1080
QY 1112 TTGCCCCCTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGGG 1171
DB 1081 TTGCCCCCTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGGG 1140
QY 1172 TTTTCTAAACGTCCTCTCTCT -CTACATAGTTGAGGAGGGGCTAGGAGTATGCTCTGG 1230
DB 1141 TTTTCTAAACGTCCTCTCTCTCTACATAGTTGAGGAGGGGCTAGGAGTATGCTCTGG 1200
QY 1231 GCGTTTCATGGGAATCATGAGATGATAATGAGAAAAATGTTATCATTTATTCATGAAG 1290
DB 1201 GCGTTTCATGGGAATCATGAGATGATAATGAGAAAAATGTTATCATTTATTCATGAAG 1260
QY 1291 TACCATTATCATTAACAATGAACCTTTATTTATTGCTCCACCAATGTTATGGGCTGAAT 1350
DB 1261 TACCATTATCATTAACAATGAACCTTTATTTATTGCTCCACCAATGTTATGGGCTGAAT 1320
QY 1351 AATGGCCCCCAAGATATCTGTGCTTAATCTCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
DB 1321 AATGGCCCCCAAGATATCTGTGCTTAATCTCTCAGAACTTGTGACTGTTACCTTCTGTG 1380

QY 1411 GCAGAAAGGAGCAGTGCAGATGCTATGTAAGTTAAGGACTTTGAGATAGAGAGGTTATTCT 1470
 Db 1381 GCAGAAAGGAGCAGTGCAGATGCTATGTAAGTTAAGGACTTTGAGATAGAGAGGTTATTCT 1440
 QY 1471 TGTGATTCAGTGGGCGCCCAATATCACCAGAGGTCCTCATAGAAAGAGGCCAGAA 1530
 Db 1441 TGTGATTCAGTGGGCGCCCAATATCACCAGAGGTCCTCATAGAAAGAGGCCAGAA 1500
 QY 1531 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTCACGTGAGCAGGG 1590
 Db 1501 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTCACGTGAGCAGGG 1560
 QY 1591 GCCATGAATGCCGCGCCTTCAGATGCCAGAAAGGGAAGGAATGATTCCTCCCTGCCTGG 1650
 Db 1561 GCCATGAATGCCGCGCCTTCAGATGCCAGAAAGGGAAGGAATGATTCCTCCCTGCCTGG 1620
 QY 1651 AGCTCCAAAGAAACCCAGCCCTGCGCCAGCTTGCATTTGAGCCCATTTGAAACTGATCTT 1710
 Db 1621 AGCTCCAAAGAAACCCAGCCCTGCGCCAGCTTGCATTTGAGCCCATTTGAAACTGATCTT 1680
 QY 1711 GAGCTCCTGCGCTCCAGATTCAGAGAGATAAATTTGTTGTTTAAATGAAAAAAA 1770
 Db 1681 GAGCTCCTGCGCTCCAGATTCAGAGAGATAAATTTGTTGTTTAAATGAAAAAAA 1740
 QY 1771 AAAAAAAGAAAAA 1786
 Db 1741 AAAAAAAGAAAAA 1756

RESULT 12
 ADB73176
 ID ADB73176 standard; cDNA; 1837 BP.
 AC ADB73176;
 XX
 XX
 XX 04-DEC-2003 (first entry)
 DE
 XX Novel human secreted and transmembrane protein PRO10111 cDNA.
 KW human; secreted and transmembrane protein; PRO; gene; ss; cytostatic;
 KW vulnary; antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumor necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumor; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003096969-A1.
 XX
 PD 22-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232223.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;
 PI Gramaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-765525/72.
 DR P-PSDB; ADB73177.
 XX
 XX New isolated PRO polypeptides useful as molecular weight markers in
 PT protein electrophoresis, useful for tissue typing, and for treating
 PT arthritis and tumors.

XX
 PS Claim 2; Fig 39; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO1725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumor necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO1341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumor in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumor in the mammal. The tumor is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This sequence encodes a human secreted and transmembrane
 CC PRO polypeptide.
 XX
 SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
 Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 QY 32 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 91
 Db 1 ACCAGCAGAGGCTGGAGTCTGTAGTTGTTCTGCTGCCAGGCTCCACTGAGGGGAAC 60
 QY 92 GGGGACCTGTCTGAAGAGAGAGATGCCCTGCTGACACTTACCTGCTCTCTTCTGGCTC 151
 Db 61 GGGGACCTGTCTGAAGAGAGAGATGCCCTGCTGACACTTACCTGCTCTCTTCTGGCTC 120
 QY 152 TCAGGCTACTCCATTGCCACTCAATACCCGCTCCAAACAGTCAATGGCTTGGAGCGG 211
 Db 121 TCAGGCTACTCCATTGCCACTCAATACCCGCTCCAAACAGTCAATGGCTTGGAGCGG 180
 QY 212 GGCTCTTGAACCGTCAAGTGTGTTTACAGATCAGGCTGGGAGACCTATTGAAGTGGTG 271
 Db 181 GGCTCTTGAACCGTCAAGTGTGTTTACAGATCAGGCTGGGAGACCTATTGAAGTGGTG 240
 QY 272 TGTGAGGAGCTATTGCGGTGACCTGCAAGATCCTTTGTTAAACCCAGTGGGTGAGGAG 331
 Db 241 TGTGAGGAGCTATTGCGGTGACCTGCAAGATCCTTTGTTAAACCCAGTGGGTGAGGAG 300
 QY 332 GAGGTGAAGAGGACCGGTGTGTCATCAAGGACATCAGAAAAACCCGACCTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGTGTGTCATCAAGGACATCAGAAAAACCCGACCTTCACTGTG 360
 QY 392 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGCTGGGAAATGAGAAACT 451
 Db 361 ACCATGGAGGATCTCATGAAACTGATGCTGACACTTACTGCTGGGAAATGAGAAACT 420

Qy 452 GGAATGACCTTGGGTCACAGTTCAAGTGAACATTGACCCAGCACCAAGTCAACCAAGAA 511
Db 421 GGAATGACCTTGGGTCACAGTTCAAGTGAACATTGACCCAGCACCAAGTCAACCAAGAA 480
Qy 512 GAACTAGAGCTCCCACTCTGACCGGCCACACATTGGAACAACAGGACAGCTCTTG 571
Db 481 GAACTAGAGCTCCCACTCTGACCGGCCACACATTGGAACAACAGGACAGCTCTTG 540
Qy 572 AAGTCTAGTCTCTCTGCGCCCTCATCTTCAACATATTTKTYGTGTGTTTGGTGGCGGC 631
Db 541 AAGTCTAGTCTCTCTGCGCCCTCATCTTCAACATATTTGCTGCTTTGGTGGCGGC 600
Qy 632 TCACTCTGGTCTGGAGATGATGAAGTACAGAGAAACAGCGGGGATGTCACAGAG 691
Db 601 TCACTCTGGTCTGGAGATGATGAAGTACAGAGAAACAGCGGGGATGTCACAGAG 660
Qy 692 CAGTCTAGTCTGGAGGCGCTCTGCTATGACAGCTGACCTGACCTGACCTGGCC 751
Db 661 CAGTCTAGTCTGGAGGCGCTCTGCTATGACAGCTGACCTGACCTGGCC 720
Qy 752 GGAACCTCCCGGAAAGGTTACCAAGATTTCTCTCTGCCAGAGTTGACCAAGTGGAA 811
Db 721 GGAACCTCCCGGAAAGGTTACCAAGATTTCTCTCTGCCAGAGTTGACCAAGTGGAA 780
Qy 812 GTGGAATATGTCACCATGGCTTCTTCCGGAAGGAGACATTTCCCTATGATCTCTGACC 871
Db 781 GTGGAATATGTCACCATGGCTTCTTCCGGAAGGAGACATTTCCCTATGATCTCTGACC 840
Qy 872 TTGGGTCTGAGGATCAGGAACCGACCTACTGCAACATGGGCGCAMCTCAGTAGCCAMCTY 931
Db 841 TTGGGTCTGAGGATCAGGAACCGACCTACTGCAACATGGGCGCACCTCAGTAGCCACCTC 900
Qy 932 CCGGCGAGGCGCTGAGGAGCCACCGAATACAGCAACATCAGCAGGCGCTTACCTGCA 991
Db 901 CCGGCGAGGCGCTGAGGAGCCACCGAATACAGCAACATCAGCAGGCGCTTACCTGCA 960
Qy 992 CTCAGGCTCTCTTGGACCCAGGCTGTGAGCACACTCTGCTCATCGACCGTCTGC 1051
Db 961 CTCAGGCTCTCTTGGACCCAGGCTGTGAGCACACTCTGCTCATCGACCGTCTGC 1020
Qy 1052 CCCTGTCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1111
Db 1021 CCCTGTCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1080
Qy 1112 TTGCCCCCTAGCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1171
Db 1081 TTGCCCCCTAGCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG 1140
Qy 1172 TTTTCTAAAGCTCCCTCTCTCTCTACATAGTTGAGGAGGGGCTAGGGATATCTCTGG 1230
Db 1141 TTTTCTAAAGCTCCCTCTCTCTCTACATAGTTGAGGAGGGGCTAGGGATATCTCTGG 1200
Qy 1231 GGCTTTCATGGAGATGATGAAGTGAATAGAGAAATGTTATCATATATCATGAAG 1290
Db 1201 GGCTTTCATGGAGATGATGAAGTGAATAGAGAAATGTTATCATATATCATGAAG 1260
Qy 1291 TACCATATCATATACATGAACCTTATTTATTTGCTTACCATGTTATGGGCTCAAT 1350
Db 1261 TACCATATCATATACATGAACCTTATTTATTTGCTTACCATGTTATGGGCTCAAT 1320
Qy 1351 AATGCCCCCAAGATATCTGTCTCTTAATCCTCAGAACCTTGTGACCTTCTCTGTG 1410
Db 1321 AATGCCCCCAAGATATCTGTCTCTTAATCCTCAGAACCTTGTGACCTTCTCTGTG 1380
Qy 1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTCT 1470
Db 1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTCT 1440
Qy 1471 TGCTGATTGAGTGGGCGCCCAAAATATACCAACAGGCTTCTCATAGAAAGAGGCCAGAA 1530
Db 1441 TGCTGATTGAGTGGGCGCCCAAAATATACCAACAGGCTTCTCATAGAAAGAGGCCAGAA 1500
Qy 1531 GGTCAAAGAGGTAGAGACAAAGTGTGATGGAAGTGGACGTGGGTGTGACGTGAGCAGG 1590

Db 1501 GGTCAAAGAGGTAGAGACAAAGTGTGATGGAAGTGGACGTGGGTGTGACGTGAGCAGG 1560
Qy 1591 GCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGAATCCCTCCCTGG 1650
Db 1561 GCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGAATCCCTCCCTGG 1620
Qy 1651 AGCTTCCAAAAGAAACACAGCCCTGCCACGGCTTGACTTGAGCCCATTTGAAACTGATCTT 1710
Db 1621 AGCTTCCAAAAGAAACACAGCCCTGCCACGGCTTGACTTGAGCCCATTTGAAACTGATCTT 1680
Qy 1711 GAGCTCTGGCTCCAGAAATTCAGAGAGAAATAATTTGTGTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCTGGCTCCAGAAATTCAGAGAGAAATAATTTGTGTGTTTAAATGAAAAAAA 1740
Qy 1771 AAAAAAAGAAAAA 1786
Db 1741 AAAAAAAGAAAAA 1756

RESULT 13
ADB78258
ID ADB78258 standard; cDNA; 1837 BP.
XX
AC ADB78258;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10111 cDNA.
XX
DE Human; secreted and transmembrane protein; PRO; gene; ss; cytostatic;
KW vulnary; antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003092889-A1.
XX
PD 15-MAY-2003.
XX
PF 13-AUG-2002; 2002US-00219478.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI P-PSDB; ADB78259.
XX
DR WPI; 2003-765495/72.
XX
DR P-PSDB; ADB78259.
XX
PT New isolated PRO polypeptide useful for tissue typing, gene therapy, as
PT molecular weight markers in protein electrophoresis, and for treating
PT arthritis and tumors.
XX
PS Claim 2; Fig 39; 308pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO382, PRO1150, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF) -

CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1403, PRO1474, PRO1917, PRO1567,
 CC PRO1887, PRO1328, PRO3431, PRO1801, PRO3333, PRO3543, PRO3444, PRO4322,
 CC PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO3402, PRO4488,
 CC PRO5723, PRO5725, PRO1154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO1174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This sequence encodes a human secreted and transmembrane
 CC PRO polypeptide.

XX
 SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match 97.0%; Score 1741.6; DB 8; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

CC	32	ACCACGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACGTGAGGGGAAC	91	541	AAGCTCAGTGTCTCTCTGCTGCCCTCATCTTACCATATTGCTGCTGCTTTTGGTGGCGGCC	600
CC	1	ACCACGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACGTGAGGGGAAC	60	542	TCACCTTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCTCCAGAG	591
CC	92	GGGACCTGTCTGAAGAGAAGATGCCCTGTGTACACTCTACCTGCTCTCTTCTGCTC	151	543	TCACCTTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCTCCAGAG	660
CC	61	GGGACCTGTCTGAAGAGAAGATGCCCTGTGTACACTCTACCTGCTCTCTTCTGCTC	120	544	CAGGTACTCAGACCCCTGGAGGGCCACCTCTGCTATGACAGCCTGACCCCTGACGTTGGCC	751
CC	152	TCAGGCTACTCCATGCGCACTCAATACCGGTCCACACAGTGAATGGCTTGGAGCGG	211	545	CAGGTACTCAGACCCCTGGAGGGCCACCTCTGCTATGACAGCCTGACCCCTGACGTTGGCC	720
CC	121	TCAGGCTACTCCATGCGCACTCAATACCGGTCCACACAGTGAATGGCTTGGAGCGG	180	546	GGAACTCCCGCGAAGGCTACCCAGAAAGCTTCTCTGCCCAGGTTGACCAAGTGGAA	780
CC	212	GGCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG	271	547	GTGGAATATGTCAACCATGGCTTCTTGGCGAAGGAGACATTTCTATGCACTCTGACC	871
CC	181	GGCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTG	240	548	GTGGAATATGTCAACCATGGCTTCTTGGCGAAGGAGACATTTCTATGCACTCTGACC	840
CC	272	TGTCAGAGAGCTATTGGCTGACTGCAAGATCTCTGTTAAACAGTGGGTGACAGCAG	331	549	TTGGGTGTGAGGATCAGAAACCGACCTACTGCAACATGGGCGACCTCAGTAGCCACCTC	900
CC	241	TGTCAGAGAGCTATTGGCTGACTGCAAGATCTCTGTTAAACAGTGGGTGACAGCAG	300	550	CCGGCAGGGGCCCTGAGGAGCCACGGAAATACAGACCATCAGCAGGCTTAGCCTGCA	960
CC	332	GAGGTGAAGAGGACCGGGTGTCCATCAAGACAAATCAGAAAAACCGCACTTCACTGTG	391	551	CTCCAGGCTCTTCTTGGACCCCGGAGCTGTGAGCACACTCTCTGCCCTCATCGACCTGTGC	1051
CC	301	GAGGTGAAGAGGACCGGGTGTCCATCAAGACAAATCAGAAAAACCGCACTTCACTGTG	360	552	CTCCAGGCTCTTCTTGGACCCCGGAGCTGTGAGCACACTCTCTGCCCTCATCGACCTGTGC	1020
CC	392	ACCATGAGGATCTCATGAAGATGATGCTGACACTTACTGCTGGTGGAAATGAGAAACT	451	553	CGCTGCTCCCTCATCAGGACCAACCGGGGACTGTGCTCTCGCTGATCAGCAGCA	1111
CC	361	ACCATGAGGATCTCATGAAGATGATGCTGACACTTACTGCTGGTGGAAATGAGAAACT	420	554	CGCTGCTCCCTCATCAGGACCAACCGGGGACTGTGCTCTCGCTGATCAGCAGCA	1080
CC	452	GGAAATGACCTTGGGGTCAAGTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT	511	555	TTGGCCCTTAGCTCTGGTTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGG	1171
CC	421	GGAAATGACCTTGGGGTCAAGTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT	480	556	TTGGCCCTTAGCTCTGGTTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGG	1140
CC	512	GAAATAGCAGCTCCCCAATCTGACCGGCCACCACTTGGCAACAGGCAACAGCTCCTG	571	557	TTTTCTAAACGTCCTCTCTCTACATAGTGTAGGAGGGGGCTAGGGATATGCTCTGG	1230
CC	481	GAAATAGCAGCTCCCCAATCTGACCGGCCACCACTTGGCAACAGGCAACAGCTCCTG	540	558	TTTTCTAAACGTCCTCTCTCTCTACATAGTGTAGGAGGGGGCTAGGGATATGCTCTGG	1200
CC	572	AAGCTCAGTGTCTCTGCTCCCTCATCTTACCATATTKYTGCTGCTTTTGGTGGCGGC	631	559	GGCTTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1290
CC				560	GGCTTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAAG	1260
CC				561	TACCATTTATAATAACAACTTTATTTATTTGGCTTACCAATGTTATGGGCTGAAT	1320
CC				562	TACCATTTATAATAACAACTTTATTTATTTGGCTTACCAATGTTATGGGCTGAAT	1350
CC				563	AATGGCCCCCAAGATATCTGCTCTAATCTCAGAACTTGTGACTGTACCTCTCTGTG	1410
CC				564	AATGGCCCCCAAGATATCTGCTCTAATCTCAGAACTTGTGACTGTACCTCTCTGTG	1380
CC				565	GCAGAAAGGGACAGTGCAGATGTAAGTAAAGTTAAGGACTTTTGGATAGAGAGTTATCT	1470
CC				566	GCAGAAAGGGACAGTGCAGATGTAAGTAAAGTTAAGGACTTTTGGATAGAGAGTTATCT	1440
CC				567	TGCTGATTCAGTGGGCCCAAAATATCACCACAGGGTCTCTATGAAGAGGCGCAGAA	1530
CC				568	TGCTGATTCAGTGGGCCCAAAATATCACCACAGGGTCTCTATGAAGAGGCGCAGAA	1500
CC				569	GGTCAAGAGGTAGAGACAAAGTGAATGAGAAAGTGGGCTGACCTGAGCAGGG	1590
CC				570	GGTCAAGAGGTAGAGACAAAGTGAATGAGAAAGTGGGCTGACCTGAGCAGGG	1560
CC				571	GCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTGCTCTGG	1650
CC				572	GCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTGCTCTGG	1620
CC				573	AGCTCCCAAGAAACACCGCCCTGCCAGCTTGGACCTTGAAGGCTTGAAGTATCTT	1710
CC				574	AGCTCCCAAGAAACACCGCCCTGCCAGCTTGGACCTTGAAGGCTTGAAGTATCTT	1680

QY 1711 GAGCTCTGGCTCCAGATTGAGGAGATAAATTTGTTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCTGGCTCCAGATTGAGGAGATAAATTTGTTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAAAAAAAA 1786
Db 1741 AAAAAAAAAAAAAA 1756
RESULT 14
ID ADB84906
XX ADB84906 standard; cDNA; 1837 BP.
AC ADB84906;
XX 04-DEC-2003 (first entry)
XX Human PRO polynucleotide #20.
XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW tumour; cancer; lung; colon; breast; prostate; rectum; liver;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW arthritis; sports injury; cytostatic; antiarthritic.
XX Homo sapiens.
OS US2003073817-A1.
XX 17-APR-2003.
XX 26-AUG-2002; 2002US-00227883.
XX 01-AUG-2000; 2000US-0222425P.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-730024/69.
XX P-PSDB; ADB84907.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX e.g. in gene therapy, disease diagnosis, chromosome identification and
XX tissue typing.
XX Claim 2; Fig 39; 314pp; English.
XX The invention relates to human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the PRO polynucleotides encoding them.
XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. They are particularly useful for
XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
XX prostate tumour, rectal tumour or liver tumour) in a mammal, for
XX stimulating the release of tumour necrosis factor (TNF)-alpha from human
XX blood, for stimulating the proliferation or differentiation of
XX chondrocyte cells, for stimulating the proliferation of or gene
XX expression in pericyte cells or for stimulating the proliferation of
XX normal human dermal fibroblasts. The PRO nucleic acids are useful as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant
XX technology, in generating transgenic animals or knock-out animals which
XX may be used in the development and screening of therapeutically useful
XX reagents, in gene therapy, in chromosome identification, as chromosome
XX markers and in generating probes. The PRO polypeptides, or anti-PRO
XX antibodies, are useful for preparing a medicament for treating a
XX condition which is responsive to the PRO polypeptides or anti-PRO
XX antibodies, such as pericyte-associated tumours and bone and/or cartilage

CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polynucleotide of the invention.
XX
SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;
Query Match 97.0%; Score 1741.6; DB 9; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGAAAC 91
Db 1 ACCAGCAGAAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGAAAC 60
QY 92 GGGACCTGTGTGAAGAGAAAGATGCCCTGTGTACACTCTACTCTCTCTCTCTCTCTCTCT 151
Db 61 GGGACCTGTGTGAAGAGAAAGATGCCCTGTGTACACTCTACTCTCTCTCTCTCTCTCTCT 120
QY 152 TCAGGCTACTCCATTGCCACTCAATACCGTCCCAACACAGTGAATGGCTTGGAGCGG 211
Db 121 TCAGGCTACTCCATTGCCACTCAATACCGTCCCAACACAGTGAATGGCTTGGAGCGG 180
QY 212 GGCTCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
Db 181 GGCTCTTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240
QY 272 TGTGAGAGAGTATTGTCGCTGACTGCAAGATCTTGTATAAACCAGTGGCTCAGAGCAG 331
Db 241 TGTGAGAGAGTATTGTCGCTGACTGCAAGATCTTGTATAAACCAGTGGCTCAGAGCAG 300
QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGACCTTCACTGTG 391
Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAGAAAAACCGACCTTCACTGTG 360
QY 392 ACCATGAGAGTCTCATGAAAACTGATGTCGACACTTACTGTGTGGAAATGAGAAAACT 451
Db 361 ACCATGAGAGTCTCATGAAAACTGATGTCGACACTTACTGTGTGGAAATGAGAAAACT 420
QY 452 GGAATGACCTTGGGGTGCAGTTCAGTGCACCTGACCTGACCGACACAGTCCACCAAGAA 511
Db 421 GGAATGACCTTGGGGTGCAGTTCAGTGCACCTGACCTGACCGACACAGTCCACCAAGAA 480
QY 512 GAACTAGCAGTCCCCCACTCTGACCGGCCACCACTTGGACAAACAGGACCAAGTCTCTG 571
Db 481 GAACTAGCAGTCCCCCACTCTGACCGGCCACCACTTGGACAAACAGGACCAAGTCTCTG 540
QY 572 AAGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
Db 541 AAGCTCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 632 TCACCTCTTGGCTTGGAGATGATGAATACCAAGAGTACCAAGAGCGCGGGATGTCCCCAGAG 691
Db 601 TCACCTCTTGGCTTGGAGATGATGAATACCAAGAGCGCGGGATGTCCCCAGAG 660
QY 692 CAGGTACTGCAGCCCTGGAGGGCGACCTCTCTCTATGAGACCTGACCTGAGCTGAGCTGCC 751
Db 661 CAGGTACTGCAGCCCTGGAGGGCGACCTCTCTCTATGAGACCTGACCTGAGCTGAGCTGCC 720
QY 752 GGAACCTCTCCCGAAAAGGCTACCAAGAGTCTCTCTGCTGCCAGGTTGACCAAGTGGAA 811
Db 721 GGAACCTCTCCCGAAAAGGCTACCAAGAGTCTCTCTGCTGCCAGGTTGACCAAGTGGAA 780
QY 812 GTGGAATATGTCAACATGCTTCTTGTGCGAAGAGGACATTTCTCTATGCACTCTCTGACC 871
Db 781 GTGGAATATGTCAACATGCTTCTTGTGCGAAGAGGACATTTCTCTATGCACTCTCTGACC 840
QY 872 TTGGGTGCTGAGATCAGGAACCGACCTTACTGCAATGGGCGCACTAGTAGGCGACMTY 931
Db 841 TTGGGTGCTGAGATCAGGAACCGACCTTACTGCAATGGGCGCACTAGTAGGCGACCTCT 900
QY 932 CCGGAGGAGGGGCTTGGAGGAGCGGCAATACAGCAATCAGCAGGCTTAGCCTGCA 991

D _b	901	CCCGCAGGGGCCCTGAGGACCCACCGAATAFACAGCACCATCAGCAGGCCTTAGCCTGCA	960
Q _y	992	CTCAGGCTCCTTCTTGGAACCCCAGGTGTGAGCACACTCCTGCTCATCGAACCGTCTGC	1051
D _b	961	CTCAGGCTCCTTCTTGACCCCAAGGTGTGAGCACACTCCTGCTCATCGAACCGTCTGC	1020
Q _y	1052	CCCGTCCTCCCTCATCAGNACCACCGGGGATGGTGCTCTGCGCTGATCAGCCAGCA	1111
D _b	1021	CCCCCTGCTCCCTCATCAGHACCACCGGGGATGTGTGCTCTGCTGATCAGCCAGCA	1080
Q _y	1112	TTCGCCCTAGTCTTGGGTGGGCTTGGGCCCAAGTCTCAGGGGCTCTTAGGAGTTGGGG	1171
D _b	1081	TTCGCCCTAGTCTTGGGTGGGCTTGGGCCCAAGTCTCAGGGGCTCTTAGGAGTTGGGG	1140
Q _y	1172	TTTTCTAAACGTCCCTCCCTCT - CTCATAGTTCAGGAGGGGCTAGGATATGCTCTGG	1230
D _b	1141	TTTTCTAAACGTCCCTCCCTCTCATAGTTGAGGAGGGGCTAGGATATGCTCTGG	1200
Q _y	1231	GGCTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTATCATATTATCATGAAG	1290
D _b	1201	GGCTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTATCATATTATCATGAAG	1260
Q _y	1291	TACCATTTATCATATACAATGAACTTTATTTATTTGCTACCCACATGTTATGGGCTCAAT	1350
D _b	1261	TACCATTTATCATATACAATGAACTTTATTTATTTGCTACCCACATGTTATGGGCTCAAT	1320
Q _y	1351	AATGGCCCCAAGATATCTGTGCTTAATCTCAGAACTTGTGACTGTGTACCTTCTGTG	1410
D _b	1321	AATGGCCCCAAGATATCTGTGCTTAATCTCAGAACTTGTGACTGTGTACCTTCTGTG	1380
Q _y	1411	GCAGAAAGGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATAGAGAGGTTATCT	1470
D _b	1381	GCAGAAAGGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATAGAGAGGTTATCT	1440
Q _y	1471	TGCTGATTGAGTGGGGCCAAAATATCACACAGAGGTCTCTATAAGAAAGAGGCCAGAA	1530
D _b	1441	TGCTGATTGAGTGGGGCCAAAATATCACACAGAGGTCTCTATAAGAAAGAGGCCAGAA	1500
Q _y	1531	GGTCAAAGAGGTAGAGACAAAGTCATATGGAAGTGCACGTGGGTGTGCACTGAGCAGGG	1590
D _b	1501	GGTCAAAGAGGTAGAGACAAAGTCATATGGAAGTGCACGTGGGTGTGCACTGAGCAGGG	1560
Q _y	1591	GCCAATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAATGGAATCCCCTGCTCTGG	1650
D _b	1561	GCCAATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAATGGAATCCCCTGCTCTGG	1620
Q _y	1651	AGCCTCCAAAGAAACCAAGCCCTGCCACAGCCTTGACTTGAGGCCCATTTGAAACTGATCTT	1710
D _b	1621	AGCCTCCAAAGAAACCAAGCCCTGCCACAGCCTTGACTTGAGGCCCATTTGAAACTGATCTT	1680
Q _y	1711	GAGCTCCTGCCTCCAGAATTCGAGGAGAAATAATTTGTGTGTTTTTATGAAAAAAA	1770
D _b	1681	GAGCTCCTGCCTCCAGAATTCGAGGAGAAATAATTTGTGTGTTTTTATGAAAAAAA	1740
Q _y	1771	AAAAAAAAAAAAAAAAAAAA 1786	
D _b	1741	AAAAAAAAAAAAAAAAAAAA 1756	

RESULT 15
ADB78012

ADB78012
ID ADB78012 standard; cDNA; 1837 BP.

XX ADB78012;

XX
DT 04-DEC-2003 (first entry)

XX
DE Novel human secreted and transmembrane protein PRO10111 cDNA.

XX Human; secreted and transmembrane protein; PRO; gene; ss; cytostatic;
KW vulnary; aniaethritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor:alpha release

KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.

XX Homo sapiens.
OS

XX
PN US2003092886-A1.

XX
PD
15-MAY-2003.

XX
PF 09-AUG-2002: 2002US-00216165.

XX
PR 25-JUL-2000: 2000US-0220607P.

PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

PA (GETH) GENENTECH INC.

PI Baker KP, Desnoyers L

XX
DR WPI; 2003-765494/72.
DR P-PSDB; ADB78013.

XX
PT Novel isolated PR

PT molecular weight markers in protein electrophoresis, for creating
PT arthritis, tumor.

XX
PS
Claim 2; Fig 39;

XX The invention des

CC polypeptide (1). PRO982, PRO1160
CC useful for stimulating the prolif-

pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO331, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) - alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO331, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1293, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567, PRO1987, PRO1328, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4332, PRO5940, PRO6079, PRO9836 or PRO10036 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblast cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This sequence encodes a human secreted and transmembrane PRO polypeptide.

XX
SQ Sequence 1837 BP; 527 A; 454 C; 465 G; 391 T; 0 U; 0 Other;

Query Match

Query Match 97.0%; Score 1741.0;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 5; Mismatches 0; Indels 1; Gaps 1;			
Qy	32	ACCAGCAGAAAGGTGGAGTCTCTAGTTTGTCTCTGCTCCAGGCTCCACTAGAGGGAAC	91
Db	1	ACCAGCAGAAAGGTGGAGTCTCTAGTTTGTCTCTGCTCCAGGCTCCACTAGAGGGAAC	60
Qy	92	GGGACCTGTCTGAAGAGAGATGCCCTGCTGACACTCTACCTGCTCTCTCTCTGCTC	151
Db	61	GGGACCTGTCTGAAGAGAGATGCCCTGCTGACACTCTACCTGCTCTCTCTCTCTGCTC	120
Qy	152	TCAGGCTACTCCATTTGCCACTCAAAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCGG	211
Db	121	TCAGGCTACTCCATTTGCCACTCAAAATCACCGGTCCAAACACAGTGAATGGCTTGGAGCGG	180
Qy	212	GGCTCTTGAACCGTGAGTGTGTTTACAGATCAGGCTGGGAGACCTTACTTGAAGTGGTG	271
Db	181	GGCTCTTGAACCGTGAGTGTGTTTACAGATCAGGCTGGGAGACCTTACTTGAAGTGGTG	240
Qy	272	TGTCAGAGAGCTATTTGGCGTGACTGCAAGATCTTGTAAACACAGTGGGTGAGAGCAG	331
Db	241	TGTCAGAGAGCTATTTGGCGTGACTGCAAGATCTTGTAAACACAGTGGGTGAGAGCAG	300
Qy	332	GAGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCAGCTTCACTGTG	391
Db	301	GAGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCAGCTTCACTGTG	360
Qy	392	ACCATGAGGATCTCATGAAATCTGATGCTGACACTTACTGTGTGGAATTGAGAAACT	451
Db	361	ACCATGAGGATCTCATGAAATCTGATGCTGACACTTACTGTGTGGAATTGAGAAACT	420
Qy	452	GGAAATGACCTTGGGGTCAAGTTCAGATGACCATTTGACCCAGCACCGAGTCAACCAAGAA	511
Db	421	GGAAATGACCTTGGGGTCAAGTTCAGATGACCATTTGACCCAGCACCGAGTCAACCAAGAA	480
Qy	512	GAACTAGAGAGTCCCACTGACCGGCGACACTTGGACACAGGACAGGCTCCCTG	571
Db	481	GAACTAGAGAGTCCCACTGACCGGCGACACTTGGACACAGGACAGGCTCCCTG	540
Qy	572	AAGTCTAGTGTCTCTGCGCCCTCATCTTCAACATATTKVTGTGCTTTTGGTGGCGCC	631
Db	541	AAGTCTAGTGTCTCTGCGCCCTCATCTTCAACATATTKVTGTGCTTTTGGTGGCGCC	600
Qy	632	TCACTTTGGTGGAGATGATGAAGTACAGCAGAAAGACCGGGATGTCCACAGAG	691
Db	601	TCACTTTGGTGGAGATGATGAAGTACAGCAGAAAGACCGGGATGTCCACAGAG	660
Qy	692	CAGTACTGACGCCCCCTGGAGGGGACCTCTGTCTATGACAGCTGACCCCTGACGCTGGCC	751
Db	661	CAGTACTGACGCCCCCTGGAGGGGACCTCTGTCTATGACAGCTGACCCCTGACGCTGGCC	720
Qy	752	GGAACTCTCCCGGAAAGGCTACCAAGATTTTCTCTGCCAGGTTGACCAAGTGGAA	811
Db	721	GGAACTCTCCCGGAAAGGCTACCAAGATTTTCTCTGCCAGGTTGACCAAGTGGAA	780
Qy	812	GTGGAATATGTACCATGGCTTCTTGGCGAGAGAGACATTTCTATGATCTCTGACC	871
Db	781	GTGGAATATGTACCATGGCTTCTTGGCGAGAGAGACATTTCTATGATCTCTGACC	840
Qy	872	TTGGGTGTGAGGATCAGGAACCGACCTACTGTCAACATGGGCCAMCTCAGTAGCCAMCTY	931
Db	841	TTGGGTGTGAGGATCAGGAACCGACCTACTGTCAACATGGGCCAMCTCAGTAGCCAMCTC	900
Qy	932	CCCGGAGGGCCCTGAGAGGCCACCGGAATACAGACCATCAGCAGGCCCTTAGCCTGCA	991
Db	901	CCCGGAGGGCCCTGAGAGGCCACCGGAATACAGACCATCAGCAGGCCCTTAGCCTGCA	960
Qy	992	CTCAGAGGCTCTTCTTGGACCCCGAGGCTGTGAGCAGACACTCTCTGCTCATGACCGTCTGC	1051
Db	961	CTCAGAGGCTCTTCTTGGACCCCGAGGCTGTGAGCAGACACTCTCTGCTCATGACCGTCTGC	1020
Qy	1052	CCCTGTCTCCCTCATCAGGACCAACCGGGGATGTGTGCTGTCTGCTGTATCAGCCAGCA	1111
Db	1021	CCCTGTCTCCCTCATCAGGACCAACCGGGGATGTGTGCTGTCTGCTGTATCAGCCAGCA	1080

Search completed: September 21, 2004, 17:18:15
Job time : 743 secs

Qy	1112	TTGCCCTAGCTCTGGGTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGAGTTGGG	1171
Db	1081	TTGCCCTAGCTCTGGGTGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGAGTTGGG	1140
Qy	1172	TTTTCTAAACGTCGCCCTCCTCT-CTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG	1230
Db	1141	TTTTCTAAACGTCGCCCTCCTCTCTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG	1200
Qy	1231	GGCTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAG	1290
Db	1201	GGCTTTCATGGGAATGATGAAGATGATATGAGAAAAATGTTATCATTTATCATGAG	1260
Qy	1291	TACCAATTAATATAATACAACTTTATTTATTTGCTACCATGTTATGGGCTGAAT	1350
Db	1261	TACCAATTAATATAATACAACTTTATTTATTTGCTACCATGTTATGGGCTGAAT	1320
Qy	1351	AATGCCCCCAAGATATCTGTGCTCTAATCCTCAGAACTTGTGACTTGTACCTTCTGTG	1410
Db	1321	AATGCCCCCAAGATATCTGTGCTCTAATCCTCAGAACTTGTGACTTGTACCTTCTGTG	1380
Qy	1411	GCAGAAAGGGACAGTCAGATGATGTAAGTTAAGGCTTTGAGATAGAGAGTTATTCT	1470
Db	1381	GCAGAAAGGGACAGTCAGATGATGTAAGTTAAGGCTTTGAGATAGAGAGTTATTCT	1440
Qy	1471	TGCTGATTCAGGTGGGCCCCAAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA	1530
Db	1441	TGCTGATTCAGGTGGGCCCCAAAATATCACCAAGGGTCTCTATAAGAAAGAGGCCAGAA	1500
Qy	1531	GGTCAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGGTGTGACGTGACGAGG	1590
Db	1501	GGTCAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGGTGTGACGTGACGAGG	1560
Qy	1591	GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCTGCTGG	1650
Db	1561	GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCTGCTGG	1620
Qy	1651	AGCCTCCAAAAGAAACCGCCCTGCCCACGCTTGACTTGAGCCCATTTGAAACTGATCTT	1710
Db	1621	AGCCTCCAAAAGAAACCGCCCTGCCCACGCTTGACTTGAGCCCATTTGAAACTGATCTT	1680
Qy	1711	GAGCTCCTGGCCTCCAGAAATTCAGAGAGATAAATTTCTGTTGTTTTTAATGAAAAAAA	1770
Db	1681	GAGCTCCTGGCCTCCAGAAATTCAGAGAGATAAATTTCTGTTGTTTTTAATGAAAAAAA	1740
Qy	1771	AAAAAAAAAAAAAAAAAAAA 1786	
Db	1741	AAAAAAAAAAAAAAAAAAAA 1756	

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 16:38:22 ; Search time 139 seconds

(without alignments)
7170.445 Million cell updates/sec

Title: US-09-997-131-19

Perfect score: 1796

Sequence: 1 ggaaggaggaagtccaagg.....aaaaaaaaaagcgccgcg 1796

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NH:*
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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	183.4	10.2	2345	3	US-08-955-937A-1
2	183.4	10.2	2345	3	US-09-300-985-1
3	176.2	9.8	708	3	US-08-955-937A-3
4	176.2	9.8	708	3	US-09-300-985-3
C 5	103	5.7	246240	2	US-08-724-394A-20
C 6	103	5.7	246240	2	US-08-724-394A-21
C 7	103	5.7	246240	2	US-08-724-394A-22
8	99.6	5.5	2103	3	US-08-897-340-2
9	99.6	5.5	2103	3	US-09-252-329-2
10	98.4	5.5	4079	4	US-09-016-434-1449
11	98.4	4.7	8758	4	US-09-799-345-3
12	84.6	4.7	8758	4	US-09-962-276-3
13	78.8	4.4	5445	4	US-09-578-458-15
C 14	75.8	4.2	128779	4	US-09-497-855A-38
15	75.6	4.2	998	4	US-09-316-081-1
16	75.6	4.2	998	4	US-09-316-081-3
17	75.6	4.2	998	4	US-09-578-458-1
18	75.6	4.2	998	4	US-09-578-458-3
19	75.6	4.2	998	4	US-09-522-964A-1
20	75.6	4.2	998	4	US-09-522-964A-3
C 21	75.4	4.2	432	4	US-09-621-976-9684
22	74	4.1	1366	4	US-09-578-458-12
23	74	4.1	1366	4	US-09-578-458-14
24	74	4.1	1366	4	US-09-522-964A-12
25	74	4.1	1366	4	US-09-522-964A-14
26	68.6	3.8	492	4	US-09-582-934-6
27	68.6	3.8	894	4	US-09-582-934-5

28	68.6	3.8	903	4	US-09-582-934-4	Sequence 4, Appli
C 29	66.6	3.7	148567	4	US-09-801-876B-3	Sequence 3, Appli
C 30	66.6	3.7	148567	4	US-10-254-869-3	Sequence 3, Appli
C 31	63.2	3.5	50000	4	US-09-146-053-4	Sequence 4, Appli
C 32	60.4	3.4	51719	4	US-09-918-686-2	Sequence 2, Appli
C 33	60.4	3.4	92139	4	US-09-918-686-1	Sequence 1, Appli
C 34	60.4	3.3	99500	4	US-09-738-096-10	Sequence 10, Appli
C 35	58.8	3.3	95042	4	US-09-784-316-3	Sequence 3, Appli
C 36	56.2	3.1	92139	4	US-09-918-886-1	Sequence 1, Appli
C 37	56	3.1	11703	3	US-08-101-886B-3	Sequence 3, Appli
C 38	55.6	3.1	460	1	US-08-474-542A-277	Sequence 277, App
C 39	55.6	3.1	460	1	US-08-474-542A-277	Sequence 277, App
C 40	54	3.0	7218	1	US-08-232-463-14	Sequence 14, Appli
41	52	2.9	1200	1	US-08-592-126-125	Sequence 125, App
42	52	2.9	1200	4	US-08-168-595-125	Sequence 125, App
43	51.8	2.9	474	4	US-09-621-976-14736	Sequence 14736, A
C 44	51.4	2.9	176373	3	US-09-128-155-17	Sequence 17, Appli
45	51.2	2.9	261	4	US-09-621-976-18330	Sequence 18330, A

ALIGNMENTS

RESULT 1

US-08-955-937A-1
; Sequence 1, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-955-937A-1

Query Match 10.2%; Score 183.4; DB 3; Length 2345;
Best Local Similarity 70.7%; Pred. No. 5.1e-41;
Matches 258; Conservative 0; Mismatches 106; Indels 1; Gaps 1;


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;
;
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
; US-08-724-394A-20

Query Match          5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;

QY 1341 TGGGCTGAATAATGCCCCCAAGGATATCTGTGCTCTAATCTCAGAACTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127

QY 1401 ACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAG 1460
Db 37126 TTACCTTATATGCAAAAGGACTTTACATGTTTAAAGTTAAGAAATTTGAGATGGGC 37067

QY 1461 AGGTTATCTTCTGCTGAGGAGGATATCTGTGCTCTAATCTCAGAACTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127

QY 1521 GAGGCGAAGGTCAAGAGGTAGAGACA-----AAGTGTATGTAAGGAGTGGACGT 1571
Db 37007 CAGGCGAAGGTCAAGAGGTAGAGACA-----AAGTGTATGTAAGGAGTGGACGT 1571

QY 1572 GGGTGTGACGTGAGCAGGAGGAGGATGATGAGTCCGAGGAGGAGGAGGAGGAGGAGG 1631
Db 36947 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1631

QY 1632 AATGGAATCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1691
Db 36887 AATGGAATCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1691

QY 1692 GCCCATTCAGAACTGATCTTGTGAGTCTTGGCTCCAGGAGGAGGAGGAGGAGGAGGAGG 1751
Db 36828 GCTCAGTGAACCCATTTTGGACTTCTGACCTTTAGAAATTTGTAATAATAATAATTTT 36769

QY 1752 TGTGTTTT 1758
Db 36768 GTGTGTGT 36762

RESULT 6
US-08-724-394A-21/c
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
```

```
;
;
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
; US-08-724-394A-21

Query Match          5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;

QY 1341 TGGGCTGAATAATGCCCCCAAGGATATCTGTGCTCTAATCTCAGAACTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127

QY 1401 ACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAG 1460
Db 37126 TTACCTTATATGCAAAAGGACTTTACATGTTTAAAGTTAAGAAATTTGAGATGGGC 37067

QY 1461 AGGTTATCTTCTGCTGAGGAGGATATCTGTGCTCTAATCTCAGAACTTGTGACTGTT 1400
Db 37186 TAGGCTGAATGTGCTCTCAAGATATCCATGCTCTAATCCCAAGACCTGTAAATATA 37127

QY 1521 GAGGCGAAGGTCAAGAGGTAGAGACA-----AAGTGTATGTAAGGAGTGGACGT 1571
Db 37007 CAGGCGAAGGTCAAGAGGTAGAGACA-----AAGTGTATGTAAGGAGTGGACGT 1571

QY 1572 GGGTGTGACGTGAGCAGGAGGAGGATGATGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGG 1631
Db 36947 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1631

QY 1632 AATGGAATCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1691
Db 36887 AATGGAATCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1691

QY 1692 GCCCATTCAGAACTGATCTTGTGAGTCTTGGCTCCAGGAGGAGGAGGAGGAGGAGGAGG 1751
Db 36828 GCTCAGTGAACCCATTTTGGACTTCTGACCTTTAGAAATTTGTAATAATAATAATTTT 36769

QY 1752 TGTGTTTT 1758
Db 36768 GTGTGTGT 36762

RESULT 7
US-08-724-394A-22/c
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111-3834
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/724,394A
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitts, Renee A.
;; REGISTRATION NUMBER: 35,136
;; REFERENCE/DOCKET NUMBER: 017957-000100
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-576-0200
;; TELEFAX: 415-576-0300
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246240 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..246240
;; OTHER INFORMATION: /note= "HLA-H.CONTIG"
;;
US-08-724-394A-22

Query Match 5.7%; Score 103; DB 2; Length 246240;
Best Local Similarity 57.6%; Pred. No. 2.5e-17;
Matches 246; Conservative 0; Mismatches 170; Indels 11; Gaps 3;

Qy 1341 TGGGCTGAATATGGCCCAAGATATCTGTCTCTAATCCTCAGAACTTTGACATGTT 1400
Db 37186 TAGGCTGAATGTTGTTCTCTCAAGATATCCATGTCCTTATCCCAAGACCTGTAATATA 37127

Qy 1401 ACCCTTCTGTGCAGAAAGGACAGTGCAGATGATGTAAGTTAAGACTTTGAGATAGAG 1460
Db 37126 TTACCTTATATGACAAAAGGACCTTACATGTTTAAATAGTTAAGAAATTTTGATGGGC 37067

Qy 1461 AGGTTATTTCTGCTGATTCAGTGGGCCCAAAATATCACCACAGGGTCTCTATAAGAAA 1520
Db 37066 AGATTTTCTGAAATTTTCAGATGGGCC - TAGTGTATATCAGAGGTCCTTATAAGAGA 37008

Qy 1521 GAGGCCAGAGGTCAGAGGTAGAGACA-----AAGTGATGATGGAAGTGGACGT 1571
Db 37007 CAGGCAGAGAGTCAGATAAGAGAAAAATACTTCAAGATGTTACACTGTCTGGCTTTAAG 36948

Qy 1572 GGGTGTGAGTGCAGAGGGCCATGAATCCCGCAGCCTTCAGTCCAGAAAGGGAAGG 1631
Db 36947 GTGGAGGAAAGGCCAAGAGCCAAAATGSCAGTGTCTCAAGCTGAAAAGAAAAGA 36888

Qy 1632 AATGATTTCCCTGCTGAGGCTCCAAAAGAAAACAGCCCTGCCCAGCCCTTGACTTGA 1691
Db 36887 AATGATTTTCCCTTAAGCCCTCTGGAGGGGCA-CAACCTTGCCCAATACCTTGATTTG 36829

Qy 1692 GCCCATGAAATGATCTTGTAGCTCTCGGCTCCAGAAATTCAGAGAAATTAATTTGTGT 1751
Db 36828 GCTCAGTGAACCCATTTTGGACTTCTGACCTTTAGATTGTAATAATAATAAATTTT 36769

Qy 1752 TGTTTT 1758
Db 36769 GTGTGT 36762

RESULT 8
US-08-897-340-2
; Sequence 2, Application US/08897340
; Patent No. 5955306
; GENERAL INFORMATION:
; APPLICANT: Gimenc, Carlos J. and Errada, Patrick, R.
; TITLE OF INVENTION: Weight Control Pathway Genes and Uses
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,340
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/715,032
; FILING DATE: 17-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-005CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2103 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-897-340-2

Query Match 5.5%; Score 99.6; DB 2; Length 2103;
Best Local Similarity 57.0%; Pred. No. 1.3e-17;
Matches 285; Conservative 0; Mismatches 199; Indels 16; Gaps 5;

Qy 1286 TGAAGTACCATTATCATATAATAACAACCTTTATTTATGCTTACCACATGTTATGGC 1345
Db 1611 TGAACACCAAACTATTATACCGAGGGTGAATAGTTTTCGCCCAAGTTGTTGTTAGG 1670

Qy 1346 TGAATATGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGTGACTGTACCTT 1405
Db 1671 CCAGTGTAGTGGCTTCCCAAGATGCCCATGTCCTTAATCCAGGAACCTGTCAAATTACCTT 1730

Qy 1406 CTGTGCAGAAAAGGACAGTGCAGATGTAATGAAGTTAAGACTTTGAGATGAGAGGTT 1465
Db 1731 GTATGGCC-AAAGGGCTTTGCAGATGTAATGAAGTTAAGACTTTTCGCCCAAGAAAT 1789

Qy 1466 ATTCTTGTGATTCAGTGGGCCCAAAATATCACCACAGGGTCTCTATAAGAAAGAGGC 1525
Db 1790 ATCCAGCTTGTTCAGAGGGCTTGTATGCTCCTCACCCTGGGTCTGTATACAGAAAGCAG 1849

Qy 1526 CAGAAGTCAAAGAGGTAGAGACAAAGTATGATGAAGTGAAGTGAAGTGGTGTGACGTGAG 1585
Db 1950 GTACCGGAGAGAGGTTG-----GAGTGTAGCGATGGAGCAGGAAACTGGAGTTGA 1902

Qy 1586 CAGGGCCATGAATGCGGAGCCTTCAGATGCCAGAAAGGAAGTGAATGATTCCTCCCTG 1645
Db 1903 GGAGGCGAGCTCAAGCCACAGAGTCCAGGCCACCTCAGAGCCAGGAAATCAT---CCCTC 1959

Qy 1646 CCTGGAGCCTCCAAAAGAAACCAGCCCTGCGCCCTTGACTTGAGCCCATTTGAAACTG 1705

Db 1960 CCACAGAGCCCTGGAGGCCCCAGCCCTGCTCCACCTGGACT--GGCTCAGTGAAGGCTA 2017
QY 1706 ATCTTGAGCTCCTGGC---CTCCAGAAATGACAGGAGATAAATTTGTGTGTTTAAATG 1762
Db 2018 ATTTTATAATTCUGCTGATTTTAGAATCTTAAGGGAATAAATTTGTGTGTTTAAATG 2077
QY 1763 AAAAAAAAAAAAAAAAAAAAAA 1782
Db 2078 AAAAAAAAAAAAAAAAAAAAAA 2097

RESULT 9
US-09-252-329-2
; Sequence 2, Application US/09252329
; Patent No. 6147192
; GENERAL INFORMATION:
; APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
; TITLE OF INVENTION: Weight Control Pathway Genes and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/252,329
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/897,340
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-005CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2103 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-09-252-329-2

Query Match 5.5%; Score 99.6; DB 3; Length 2103;
Best Local Similarity 57.0%; Pred. No. 1.3e-17;
Matches 285; Conservative 0; Mismatches 199; Indels 16; Gaps 5;
QY 1286 TGAAGTACCATATCATATATCATATGCTCTATCTATCTCAGAACTTGTGACTTTACCTT 1405
Db 1611 TGAACACCAAACTATATACCGAGGGTGTATAGTTTGTGCGCACTTGTGTAGG 1670
QY 1346 TGAATAATGGCCCCCAAGATATCTGTCTCTATCTCAGAACTTGTGACTTTACCTT 1405
Db 1671 CCAGTAGTGGCTCCCAAGATGCCATGTCTCTATCCAGCACTGTCAAAATACCTT 1730
QY 1406 CTGTGGCAGAGGAGGACAGTGCAGATGTATGTAAGTAAAGACTTTGAGATAGAGGTT 1465
Db 1731 GTATGGCC-AAAGGGGCTTTGCAGATGTATGTAAGTAAAGGATCTTTCGCCAGGAAGAT 1789
QY 1466 ATTCTTGCTGATTGAGTGGGCCCCAAAATATCACCACCAAGGGTCTCTATAAGAAAGAGGC 1525

Db 1790 ATCCAGCTGTTTCAGAGGGCTTGATGTCTCCTCACCGGGTCTGTATAACAGAGAGCAG 1849
QY 1526 CAGAAGGTCAAGAGGTAGACAAAAGTGTATGTAAGTGGACGTGGGTGTGACCTGAG 1585
Db 1850 GTACCGGAGAGAGAGGTTG-----GAGGTGTAGCGATGGAGCAGAGAACTGGAGTTGA 1902
QY 1586 CAGGGGCATGAATGCGCAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCTG 1645
Db 1903 GGAGGCGAGCTCAAGCCACAGAGTCCAGGCCCTCAGAGCCAGGAATGCAT---CCTC 1959
QY 1646 CTGGAGCCTCCAAAAGAAACAGCCCTGCCCCAGCCTTGACTTGAGCCCATGAAATG 1705
Db 1960 CCACAGAGCCTGGAAAGGCCCCAGCCCTGCTCCACCTGGACT--GGCTCAGTGAAGCTA 2017
QY 1706 ATCTTGAGCTCCTGGC---CTCCAGAAATGACAGGAGATAAATTTGTGTGTTTAAATG 1762
Db 2018 ATTTTATAATTCUGCTGATTTTAGAATCTTAAGGGAATAAATTTGTGTGTTTAAATG 2077
QY 1763 AAAAAAAAAAAAAAAAAAAAAA 1782
Db 2078 AAAAAAAAAAAAAAAAAAAAAA 2097

RESULT 10
US-09-016-434-1449
; Sequence 1449, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1449:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9727358
US-09-016-434-1449

Query Match

5.5%; Score 98.4; DB 4; Length 4079;

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Best Local Similarity 60.2%; Pred. No. 4.2e-17;
Matches 201; Conservative 0; Mismatches 126; Indels 7; Gaps 2;

Qy 1430 ATGTATGTAAGTTAAGACCTTCAGATAGAGAGGTTATCTTGTGATTCAGGTGGGCC 1489
Db 3712 ATGTTACCAATTAAGGCTCTTGATGGGAGATGATCTGAATATCAAGTGGGCC 3771
Qy 1490 AAATATCACACAAGGCTCTCATAGAAAGAGGCCAGAGGTCAAAGGTAGAGACA 1549
Db 3772 --TATATAATCACAAAGGCTCTTATAGAGGAGGCGAGGAGGCTCAGAGTATGT 3829
Qy 1550 AAGTGATGATGGAAGTGCAGTGGGTGTGACGTGAGCA-----GGGSCCATGAATGCCG 1604
Db 3830 GACTATGAAACAGAGAGCCAGAGGAATTCAGGACGGCCACTAGAGCCAGGATTCGAGG 3889
Qy 1605 AGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCCTGGAGCCTCCAAAAGAA 1664
Db 3890 CACCCTCTAGAGGCTGTAAAGGCAAGAAATGGCTTCTCCCTGGAGCCTCCAGAAGGA 3949
Qy 1665 ACAGCCCTGCCAGCCTTGACTTGAGCCCATGAACTGAACTGATCTTGAAGTCTGCGCTC 1724
Db 3950 ATGGGTCTGCGCAACTCCCTGTCTTCAGCCAGGAAACAGATTTAGGATTTCTGGCCTC 4009
Qy 1725 CAGAAATGCAGCAGATAAAATTTGTTGTTTTT 1758
Db 4010 CAGAACTGTTAGAGGATACATTGTTGTTT 4043

RESULT 11
US-09-799-345-3
; Sequence 3, Application US/09799345
; Patent No. 6323016
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001156
; CURRENT APPLICATION NUMBER: US/09/799,345
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8758
; TYPE: DNA
; ORGANISM: Human
US-09-799-345-3

Query Match 4.7%; Score 84.6; DB 4; Length 8758;
Best Local Similarity 69.3%; Pred. No. 4.8e-13;
Matches 115; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1603 GCAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCCTGGAGCCTCCAAAAG 1662
Db 3859 GCGGCCACAGACGCTGAAGATGTTAGGACATGATCTCCCTCAGAGCCTCCAAAAG 3918
Qy 1663 AAACAGCCTGCCAGCCTTGACTTGAGCCCATGAACTGAACTGATCTTGAAGTCTGCGC 1722
Db 3919 AAAACAGTCTGCTGACACCTTGACTCTAGACCAGTGAAGTGGCTTTGGGCTTCTGACC 3978

RESULT 12
US-09-962-276-3
; Sequence 3, Application US/09962276
; Patent No. 6630336
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001156DIV
; CURRENT APPLICATION NUMBER: US/09/962,276
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/210,458
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/799,345
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8758
; TYPE: DNA
; ORGANISM: Human
US-09-962-276-3

Query Match 4.7%; Score 84.6; DB 4; Length 8758;
Best Local Similarity 69.3%; Pred. No. 4.8e-13;
Matches 115; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1603 GCAGCCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCTCCCTGGAGCCTCCAAAAG 1662
Db 3859 GCGGCCACAGACGCTGAAGATGTTAGGACATGATCTCCCTCAGAGCCTCCAAAAG 3918
Qy 1663 AAACAGCCTGCCAGCCTTGACTTGAGCCCATGAACTGAACTGATCTTGAAGTCTGCGC 1722
Db 3919 AAAACAGTCTGCTGACACCTTGACTCTAGACCAGTGAAGTGGCTTTGGGCTTCTGACC 3978

RESULT 13
US-09-578-458-15
; Sequence 15, Application US/09578458
; Patent No. 6365726
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-578-458-15

Query Match 4.4%; Score 78.8; DB 4; Length 5445;
Best Local Similarity 54.0%; Pred. No. 1.5e-11;
Matches 230; Conservative 0; Mismatches 187; Indels 9; Gaps 3;

Qy 1336 TGTATGGGCTGAATTAATGGCCCCC-AAAGATATCTGTCTCTTAATCTCAGAACCTGTG 1394
Db 5023 TATGGTAGGCAATAATATGCCCCCGAAATATGTCCACATCTTAATCCCAAGATCTGTGC 5082
Qy 1395 ACTGTTACCTTCTGTGGCAGAAAGGAGGACAGTGCAGATGTATGTAGTTAAGGACTTTGAG 1454
Db 5083 ATATGTTACCATACATGTCCAAAGAGGTTTGCATATGATTTATCTTAAGATCTTGAA 5142
Qy 1455 ATAGAGAGGTTATCTTGTGTGATTCAGTGGGCCCCCAAAATATCACCACAGGGTCTCAT 1514

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Db 5143 ATGAGGAGACAATCTGGGTTATCTGTGGGCTCAGTTTAAATCACAAGAGGAGGAGG 5202
Qy 1515 AAGAAAGAGGCGAGAGGTCAAGAGGTAGAGACAAAGTGATGATGGAAGTGGAGCTGGG 1574
Db 5203 AAGGAGAGAGTCAGAGAGAGATGGAAGATACCATGCTTCTAATTTTGAAGAT-----GG 5256
Qy 1575 TGTGAGCTGAGCAGGCGCATGAATGCCGCGAGCTTCAGATGCCAGAAAGGAGGAAT 1634
Db 5257 AGTGAGGCGCTTGAGCCAAATGCAAGTGTGTTTAAAGGTGGAAGAAAGCAGGAA 5316
Qy 1635 GGATTCCTCGCTGGAGCTCCAAAAGAAACAGCCCTGCCAGCCCTTGACTTTGAGCC 1694
Db 5317 CGGATTCCTCTAGAGTCTCGGAAGGAACACAGCTCT--TGACACATGATTCAGCT 5374
Qy 1695 CATTGAACTGATCTTGAGCTCTCGGCTCCAGATTCGAGAGNATAAATTTGTTGT 1754
Db 5375 CAGTGACACCCATTCAGACTTCTGACCTCCACAACTATAAAATAAATTTGTTGT 5434
Qy 1755 TTTTAA 1760
Db 5435 TGTAAA 5440

RESULT 14
US-09-497-855A-38/c
; Sequence 38, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UM01523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-38

Query Match 4.2%; Score 75.8; DB 4; Length 128779;
Best Local Similarity 57.2%; Pred. No. 7e-10;
Matches 242; Conservative 0; Mismatches 162; Indels 19; Gaps 5;

Qy 1349 ATATGGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTTGACTGTACCTTCTG 1408
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Qy 1409 TGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGACTTTTCAGATAGAGGTTATT 1468
Db 96206 TTGCACAGACCCCAAGAGGGGTCT--TCGAGAAAGTTAAGATGAGAAATTATC 96148
Qy 1469 CTGCTGATTCAGTGGGCCCAAAATATCACCAAGGGTCTCATGAAGAAAGGCCAG 1528
Db 96147 CTGATTTATCAAGTGGAGCTCAAAATACCATCAAGTGCCTTTAATAGGAGAGGCACA 96088
Qy 1529 AAGGTCA-----AAGAGGTAGACAAAGATGATGTAAGTGGAGTGGGT 1575
Db 96087 GGGAGATTATACGTTACAGAAAGAGAGAGCAATGTGCCACACCGACACAGATAGAA 96028
Qy 1576 GTGAGTGCAGAGGGGCCATGAATGCC--GAGCTTCAGATGCCAGAAAGGAAAGGAA 1633
Db 96027 GCAATGCCACCAACAGCCAGGAATCGAGAGCCACAGAGGCTGGGAAAGGTAGGA 95968
Qy 1634 TGGATTCCCTCGCTGGAGCTCCAAAAGAAC--AGCCCTGCCAGCCTTGACTTGAG 1692
Db 95967 CATATTCTTC--CTTAGAGCTTCGGAGGAGGAGTAGCCCTGCCAACACCTTGATTCAA 95910

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Db 95909 ACCAGTGATCTAGTGTGGACTTTTGGCTCCAGAACTGTGAGAAAGAGTCACTTAT 95850
Qy 1753 GTT 1755
Db 95849 TTT 95847

RESULT 15
US-09-316-081-1
; Sequence 1, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(512)
US-09-316-081-1

Query Match 4.2%; Score 75.6; DB 4; Length 998;
Best Local Similarity 53.5%; Pred. No. 4.3e-11;
Matches 228; Conservative 0; Mismatches 189; Indels 9; Gaps 3;

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Qy 1395 ACTGTTACCTTCTGTGGCAGAAAGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAG 1454
Db 634 ATATGTTACCATACATGTCCAAAGAGTTTGCAAATGTGATTATGTTAAGGATCTTGA 693
Qy 1455 ATAGAGAGTTATCTTGTGTGATTCAGGTGGGCCCAAAATATCACCAAGGCTCTCAT 1514
Db 694 ATGAGGAGACAATCTCTGGGTTATCTTGTGGGCTCAGTTTAATCAAGAAGGAGGAGG 753
Qy 1515 AAGAAGAGGCGCAGAGGTCAAGAGGTAGACACAAAGTGTATGTAAGTGGAGTGGAGTGGG 1574
Db 754 AAGGAGAGTGCAGAGAGAGATGGAAGATACCTGCTTCTAATTTGAAGAT-----GG 807
Qy 1575 TGTGAGTGCAGAGGCGCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGGAAT 1634
Db 808 AGTGAGGCGCTTGAGCCAAACATATGCAAGTGTGTTTAAAGGAGGAAAGGAGGAA 867
Qy 1635 GGATTCCTCGCTCGAGCCTCCAAAGAACACAGCCCTGCCAGCCTTGACTTGAGCC 1694
Db 868 CGGATTCCTCTATAGTCTCCGGAAGGAACACAGCTCT--TGACATATGATTTCACT 925
Qy 1695 CATTGAAACTGATCTTGAGCTCTCGGCTCCAGAAATTCAGAGAGATAAATTTGTGTGT 1754
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Qy 1755 TTTTAA 1760
Db 986 TGTAAA 991

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 17:18:23 ; Search time 868 Seconds

(without alignments)
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Title: US-09-997-131-19

Perfect score: 1796

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Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1741.6	97.0	1837	13	US-10-219-535-39 Sequence 39, Appl
2	1741.6	97.0	1837	13	US-10-232-230-39 Sequence 39, Appl
3	1741.6	97.0	1837	13	US-10-232-224-39 Sequence 39, Appl
4	1741.6	97.0	1837	15	US-10-227-884-39 Sequence 39, Appl
5	1741.6	97.0	1837	15	US-10-230-163-39 Sequence 39, Appl
6	1741.6	97.0	1837	15	US-10-230-338-39 Sequence 39, Appl
7	1741.6	97.0	1837	15	US-10-218-631-39 Sequence 39, Appl
8	1741.6	97.0	1837	15	US-10-230-414-39 Sequence 39, Appl
9	1741.6	97.0	1837	15	US-10-216-159A-39 Sequence 39, Appl
10	1741.6	97.0	1837	15	US-10-218-849-39 Sequence 39, Appl
11	1741.6	97.0	1837	15	US-10-227-873-39 Sequence 39, Appl
12	1741.6	97.0	1837	15	US-10-227-883-39 Sequence 39, Appl
13	1741.6	97.0	1837	15	US-10-219-076-39 Sequence 39, Appl
14	1741.6	97.0	1837	15	US-10-230-434-39 Sequence 39, Appl

15 1741.6 97.0 1837 15 US-10-219-003-39 Sequence 39, Appl
16 1741.6 97.0 1837 15 US-10-219-075-39 Sequence 39, Appl
17 1741.6 97.0 1837 15 US-10-219-464-39 Sequence 39, Appl
18 1741.6 97.0 1837 15 US-10-219-466-39 Sequence 39, Appl
19 1741.6 97.0 1837 15 US-10-219-479-39 Sequence 39, Appl
20 1741.6 97.0 1837 15 US-10-219-481-39 Sequence 39, Appl
21 1741.6 97.0 1837 15 US-10-230-260-39 Sequence 39, Appl
22 1741.6 97.0 1837 15 US-10-232-233-39 Sequence 39, Appl
23 1741.6 97.0 1837 15 US-10-232-233-39 Sequence 39, Appl
24 1741.6 97.0 1837 15 US-10-216-165-39 Sequence 39, Appl
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28 1741.6 97.0 1837 15 US-10-219-536-39 Sequence 39, Appl
29 1741.6 97.0 1837 15 US-10-233-205-39 Sequence 39, Appl
30 1741.6 97.0 1837 15 US-10-219-072-39 Sequence 39, Appl
31 1741.6 97.0 1837 15 US-10-219-470-39 Sequence 39, Appl
32 1741.6 97.0 1837 15 US-10-219-474-39 Sequence 39, Appl
33 1741.6 97.0 1837 15 US-10-219-524-39 Sequence 39, Appl
34 1741.6 97.0 1837 15 US-10-219-528-39 Sequence 39, Appl
35 1741.6 97.0 1837 15 US-10-227-880-39 Sequence 39, Appl
36 1741.6 97.0 1837 15 US-10-227-881-39 Sequence 39, Appl
37 1741.6 97.0 1837 15 US-10-227-882-39 Sequence 39, Appl
38 1741.6 97.0 1837 15 US-10-230-436-39 Sequence 39, Appl
39 1741.6 97.0 1837 15 US-10-232-223-39 Sequence 39, Appl
40 1741.6 97.0 1837 15 US-10-232-225-39 Sequence 39, Appl
41 1741.6 97.0 1837 15 US-10-232-227-39 Sequence 39, Appl
42 1741.6 97.0 1837 15 US-10-232-229-39 Sequence 39, Appl
43 1741.6 97.0 1837 15 US-10-232-234-39 Sequence 39, Appl
44 1741.6 97.0 1837 15 US-10-219-060-39 Sequence 39, Appl
45 1741.6 97.0 1837 15 US-10-216-160-39 Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-10-219-535-39 ; Sequence 39, Application US/10219535
; Publication No. US20040044179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C60
; CURRENT APPLICATION NUMBER: US/10/219,535
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25


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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3530F1C103
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-232-230-39

Query Match          97.0%; Score 1741.6; DB 13; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 17

Qy 32 ACCAGCAGAAGCGTGGGAGTCTGTAGTTTGTTCCTGTGCGAGGCTCCACTGAGGGGAAAC 91
Db 1 ACCAGCAGAAGCGTGGGAGTCTGTAGTTTGTTCCTGTGCGAGGCTCCACTGAGGGGAAAC 60

Qy 92 GGGGACCTGTCTGAGAGAAGATGCCCTGCTGCACACTCTACCTGTCTCCTCTTCTGGCTC 151
Db 61 GGGGACCTGTCTGAGAGAAGATGCCCTGCTGCACACTCTACCTGTCTCCTCTTCTGGCTC 120

Qy 152 TCAGGCTACTCCATTGCCACTCAATATCACCGGTCCAAACACAGTGAATGGCTTGAGCGG 211
Db 121 TCAGGCTACTCCATTGCCACTCAATATCACCGGTCCAAACACAGTGAATGGCTTGAGCGG 180

Qy 212 GGTCTCTTGACCGTGCAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGTGG 271
Db 181 GGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGCTGGGAGACCTACTTGAAGTGTGG 240

Qy 272 TGTGAGGAGCTATTGTGGCGTGACTGCAAGATCCCTTTGTTAAACCAGTGGGTTCAGACGAG 331
Db 241 TGTGAGGAGCTATTGTGGCGTGACTGCAAGATCCCTTTGTTAAACCAGTGGGTTCAGACGAG 300

Qy 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACGTTCACTGTG 391
Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGCACGTTCACTGTG 360

Qy 392 ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGTGTGGAAATTCAGAAAACT 451
Db 361 ACCATGGAGGATCTCATGAAAACTGATGCTGACACTTACTGTGTGGAAATTCAGAAAACT 420

Qy 452 GGAAATGACCTTGGGGTCCAGTTCAAGTGCACCTTTGACCCAGCCAGTACCCAGAA 511

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Db 1501 GGTCAAGAGGTTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTGACGTGAGCAGGG 1560
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RESULT 3

US-10-232-224-39
; Sequence 39, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/232,224
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-232-224-39

Query Match 97.0%; Score 1741.6; DB 13; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

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32 ACCAGCAGAGGCTGGAGTCTGTAGTTTCTCTGCTGCCAGGCTCCACTGAGGGGAAC 91

Db 1 ACCAGCAGAGGCTGGAGTCTGTAGTTTCTCTGCTGCCAGGCTCCACTGAGGGGAAC 60
QY 92 GGGGACTCTGTGAAGAGAGATGCCCCGTGCTGACACTCTACTGCTCTCTTCTGGCTC 151
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QY 212 GGCTCTTCAGCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
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Db 721 GGAACTCTCCCGGAAAGGCTACCACGAAGCTTTCTCTGCCAGGTTGACCAGGTGGAA 780
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1231 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTTATCATGAAG 1290
1201 GGCTTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATATTTATCATGAAG 1260
1291 TACCATATCATATCAATGACCTTTATTTATTCCTTACCAATGTTATGGCTGAAT 1350
1261 TACCATATCATATCAATGACCTTTATTTATTCCTTACCAATGTTATGGCTGAAT 1320
1351 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1410
1321 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTTCT 1470
1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTTCT 1440
1471 TGCTGATTCAGGTGGGCCCCAAAATATCACCACAAAGGCTCTCTATAAGAAAGAGCCAGAA 1530
1441 TGCTGATTCAGGTGGGCCCCAAAATATCACCACAAAGGCTCTCTATAAGAAAGAGCCAGAA 1500
1531 GGTCAAGAGGTGAGACAAAGTATGATGGAAGTGAAGTGGTGTGACGTGACGACAGG 1590
1501 GGTCAAGAGGTGAGACAAAGTATGATGGAAGTGAAGTGGTGTGACGTGACGACAGG 1560
1591 GCCATGAATCCGAGCCTTCAGATGCCAGAAAGGAAAGGAAATGATTCCTCTGCTCTGG 1650
1561 GCCATGAATCCGAGCCTTCAGATGCCAGAAAGGAAAGGAAATGATTCCTCTGCTCTGG 1620
1651 AGCTTCCAAAGAAACAGCCCTGCCACCCCTTGACTTGAGCCCAATGAAATGATCTT 1710
1621 AGCTTCCAAAGAAACAGCCCTGCCACCCCTTGACTTGAGCCCAATGAAATGATCTT 1680
1711 GAGTCTCTGCTCCAGAAATGAGGAGATAATTTGCTGCTTTTATGAAAAA 1770
1681 GAGTCTCTGCTCCAGAAATGAGGAGATAATTTGCTGCTTTTATGAAAAA 1740
1771 AAAAAAAAAAAAAA 1786
1741 AAAAAAAAAAAAAA 1756

RESULT 4
US-10-227-884-39
; Sequence 39, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287

, PRIOR APPLICATION NUMBER: 60/100385
 , PRIOR FILING DATE: 1998-09-15
 , PRIOR APPLICATION NUMBER: 60/100390
 , PRIOR FILING DATE: 1998-09-15
 , PRIOR APPLICATION NUMBER: 60/100627
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 , PRIOR APPLICATION NUMBER: 60/134287

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 , PRIOR APPLICATION NUMBER: 60/140650
 , PRIOR FILING DATE: 1999-06-22
 , PRIOR APPLICATION NUMBER: 60/140723
 , PRIOR FILING DATE: 1999-06-22
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 , PRIOR FILING DATE: 1999-08-31
 , PRIOR APPLICATION NUMBER: 60/164418
 , PRIOR FILING DATE: 1999-11-09
 , PRIOR APPLICATION NUMBER: 60/166361
 , PRIOR FILING DATE: 1999-11-16
 , PRIOR APPLICATION NUMBER: 60/169445
 , PRIOR FILING DATE: 1999-12-07
 , PRIOR APPLICATION NUMBER: 60/169495
 , PRIOR FILING DATE: 1999-12-07
 , PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY	32	ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTGTGCTCCAGGCTCCACGTGAGGGGAAAC	91
DB	1	ACCAGCAGAGGCTGGAGTCTGTAGTTTGTCTGTGCTCCAGGCTCCACGTGAGGGGAAAC	60
QY	92	GGGACCTGTCTGAAGAGAGATGCCCTGTGTACACTTCTACCTGCTCTCTTTCTGGTCT	151
DB	61	GGGACCTGTCTGAAGAGAGATGCCCTGTGTACACTTCTACCTGCTCTCTTTCTGGTCT	120
QY	152	TCAGGCTACTCCATTGCCACTCAATCAACGGTCCACAGCAAGTGAATGGCTTGGAGCGG	211
DB	121	TCAGGCTACTCCATTGCCACTCAATCAACGGTCCACAGCAAGTGAATGGCTTGGAGCGG	180
QY	212	GGCTCCTTTGACCGTCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	271
DB	181	GGCTCCTTTGACCGTCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG	240
QY	272	TGTCAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTATAAACAGTGGGTCAGAGCAG	331
DB	241	TGTCAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTATAAACAGTGGGTCAGAGCAG	300
QY	332	GAGGTGAAGAGGACCGGGTGTCCATCAAGGACCAATCAGAAAAACCGCACCTTCACTGTG	391
DB	301	GAGGTGAAGAGGACCGGGTGTCCATCAAGGACCAATCAGAAAAACCGCACCTTCACTGTG	360
QY	392	ACCATGGAGGATCTCATGAAAACTGATGTGACACTTACTGGTGTGGAATGGAATAACT	451
DB	361	ACCATGGAGGATCTCATGAAAACTGATGTGACACTTACTGGTGTGGAATGGAATAACT	420
QY	452	GGAATGACCTTTGGGTTCACAGTTCAAGTGACCAATTCAGCCAGACCCAGTCCACCAAGAA	511
DB	421	GGAATGACCTTTGGGTTCACAGTTCAAGTGACCAATTCAGCCAGACCCAGTCCACCAAGAA	480
QY	512	GAAACTAGCAGCTCCCAACTTCTGACCGGCAACCACTTGGACCAACAGGCAACAGCTCCTG	571
DB	481	GAAACTAGCAGCTCCCAACTTCTGACCGGCAACCACTTGGACCAACAGGCAACAGCTCCTG	540
QY	572	AAGCTCAGTGTCTCTGGCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCCGCC	631

Db 541 AAGCTCAGTGTCTCTCTGCCCCCTCATCTTACCATATTTGCTGCTGCTTTTGGTGGCCGCC 600
Qy 632 TCATCTTTGGCTTGGAGATGATGAAGTACCGACAGAAAGCAGCCGGGATGTCCTCCAGAG 691
Db 601 TCATCTTTGGCTTGGAGATGATGAAGTACCGACAGAAAGCAGCCGGGATGTCCTCCAGAG 660
Qy 692 CAGGTACTGACGCCCTGGAGGCGGACCTCTGCTATGCGACCTGACCTGACCTGACCTGGCC 751
Db 661 CAGGTACTGACGCCCTGGAGGCGGACCTCTGCTATGCGACCTGACCTGACCTGACCTGGCC 720
Qy 752 GGAACCTCCCGGAAAGGCTACCAAGAGTTTCTCTGCGCAGGTTGACCCAGGTGGAA 811
Db 721 GGAACCTCCCGGAAAGGCTACCAAGAGTTTCTCTGCGCAGGTTGACCCAGGTGGAA 780
Qy 812 GTGGATATGTCACCATGGCTTCTCTGCGAAGGAGCATTTTCCATGATCTCTGACC 871
Db 781 GTGGATATGTCACCATGGCTTCTCTGCGAAGGAGCATTTTCCATGATCTCTGACC 840
Qy 872 TTGGGTGCTGAGGATCAGGAACGACCTACTGCAACATGCGGCGCAGTCTAGTACCCAMCTY 931
Db 841 TTGGGTGCTGAGGATCAGGAACGACCTACTGCAACATGCGGCGCAGTCTAGTACCCACCTC 900
Qy 932 CCGGCGAGGGGCTGAGGAGGCCACCGAATACAGCACCATCAGCAGGCTTAGCCCTGCA 991
Db 901 CCGGCGAGGGGCTGAGGAGGCCACCGAATACAGCACCATCAGCAGGCTTAGCCCTGCA 960
Qy 992 CTCAGGCTCTCTTGGACCCCGAGGCTGTGAGCACACTCTGCTCATCGACCGCTCTGC 1051
Db 961 CTCAGGCTCTCTTGGACCCCGAGGCTGTGAGCACACTCTGCTCATCGACCGCTCTGC 1020
Qy 1052 CCCTGTCTCCCTCATCAGAACCAACCCGGGAGCTGGTGCTCTGCTGATCAGCCAGCA 1111
Db 1021 CCCTGTCTCCCTCATCAGAACCAACCCGGGAGCTGGTGCTCTGCTGATCAGCCAGCA 1080
Qy 1112 TTGCCCCAGCTCTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1171
Db 1081 TTGCCCCAGCTCTGGGCTTGGGCGCAAGTCTCAGGGGCTTCTAGGAGTTGGGG 1140
Qy 1172 TTTTCTAAAGCTCCCTCTCTCTACATAGTTAGGAGGGGCTAGGATATGCTCTGG 1230
Db 1141 TTTTCTAAAGCTCCCTCTCTCTACATAGTTAGGAGGGGCTAGGATATGCTCTGG 1200
Qy 1231 GGCTTTTATGGGATGATGAAGATGAATAGAGAAATGTTATCATTTATCATGAAG 1290
Db 1201 GGCTTTTATGGGATGATGAAGATGAATAGAGAAATGTTATCATTTATCATGAAG 1260
Qy 1291 TACCATTTATCATATACAATGAACCTTTATTTATGCTTACCACCATCTTATGGGCTGAAT 1350
Db 1261 TACCATTTATCATATACAATGAACCTTTATTTATGCTTACCACCATCTTATGGGCTGAAT 1320
Qy 1351 AATGGCCCCAAGATATCTGTCTCTTAATCTCAGAACCTTGTGACTGTACCTCTCTGG 1410
Db 1321 AATGGCCCCAAGATATCTGTCTCTTAATCTCAGAACCTTGTGACTGTACCTCTCTGG 1380
Qy 1411 GCAGAAAGGACGTGAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTTCT 1470
Db 1381 GCAGAAAGGACGTGAGATGATGTAAGTTAAGGACTTTGAGATAGAGGTTATTTCT 1440
Qy 1471 TGCTGATTCAGGTGGGCCCCAAAATATACCAAGGCTCTCATAGAAAGAGGCCAGAA 1530
Db 1441 TGCTGATTCAGGTGGGCCCCAAAATATACCAAGGCTCTCATAGAAAGAGGCCAGAA 1500
Qy 1531 GGTCAAGAGGTAGAGCAAGATGATGATGAAGTGGACGTGGGTGTGAGTGAAGCAGGG 1590
Db 1501 GGTCAAGAGGTAGAGCAAGATGATGATGAAGTGGACGTGGGTGTGAGTGAAGCAGGG 1560
Qy 1591 GCCATGAATGCCGAGCCCTCAGATGCGCAGAAAGGAAAGGATTCCTTCCCTGCTGG 1650
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Qy 1651 AGCTTCCAAAAGAAACAGCCCTGCCAGGCTTGACTTGACCCCATGAACCTGATCTT 1710
Db 1621 AGCTTCCAAAAGAAACAGCCCTGCCAGGCTTGACTTGACCCCATGAACCTGATCTT 1680

Qy 1711 GAGCTCTGGCTCCAGATTCAGAGAAATAAATTTGTTGTTTAAATGAAAAAA 1770
Db 1691 GAGCTCTGGCTCCAGATTCAGAGAAATAAATTTGTTGTTTAAATGAAAAAA 1740
Qy 1771 AAAAAA 1786
Db 1741 AAAAAA 1756

RESULT 5
US-10-230-163-39
; Sequence 39, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/064103
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; PRIOR FILING DATE: 1998-12-15
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 ; PRIOR FILING DATE: 1999-11-16
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 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY

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QY	92	GGGGAACCTGTCTGAAGAGAGAGATGCCCTCTGCTGACACTCTACTCTCTCTCTTTTGGGTC	151
D5	61	GGGGAACCTGTCTGAAGAGAGATGCCCTCTGCTGACACTCTACTCTCTCTCTTTGGGTC	120
QY	152	TCAGGCTACTCCATTTGCCACTCAATTCACGGGTCCAACCAACAGTGAATGGCTTTGAGCGG	211
D5	121	TCAGGCTACTCCATTTGCCACTCAATTCACGGGTCCAACCAACAGTGAATGGCTTTGAGCGG	180
QY	212	GGTCTCTTGACCGTCAGTGTGTTTACAGATCAGGCTGGGAGACCTTACTTGAAGTGTGG	271
D5	181	GGTCTCTTGACCGTCAGTGTGTTTACAGATCAGGCTGGGAGACCTTACTTGAAGTGTGG	240
QY	272	TGTCGAGGAGCTATTTGGCGTGACTGGAAGATCTCTTGTAAACCAAGTGGGTTCAGAGCA	331
D5	241	TGTCGAGGAGCTATTTGGCGTGACTGGAAGATCTCTTGTAAACCAAGTGGGTTCAGAGCA	300
QY	332	GAGGTGAAGAGGACCGGGTCCATCAAGGACAATCAGAAAAACCGCACGTTCACTGTG	391
D5	301	GAGGTGAAGAGGACCGGGTCCATCAAGGACAATCAGAAAAACCGCACGTTCACTGTG	360
QY	392	ACCATGGAGGATCTCATGAAAACTGATGTGACACTTACTGTGTGGAATTTGAAAAACT	451
D5	361	ACCATGGAGGATCTCATGAAAACTGATGTGACACTTACTGTGTGGAATTTGAAAAACT	420
QY	452	GGAAATCAGCTTGGGGTCAGGTTCAAGTGACCACTTGAACCCAGCACAGTCAACCAAGAA	511
D5	421	GGAAATCAGCTTGGGGTCAGGTTCAAGTGACCACTTGAACCCAGCACAGTCAACCAAGAA	480
QY	512	GAAACTAGCAGCTCCCCAACTCTGACCGGCCACACTTGGACAACAGGACAAGTCTCTG	571
D5	481	GAAACTAGCAGCTCCCCAACTCTGACCGGCCACACTTGGACAACAGGACAAGTCTCTG	540
QY	572	AAGCTCAGTGTCTCTGCCCCCATCTTCAACCATATTXTGTGTCTTTTGGTGGCGGCC	631
D5	541	AAGCTCAGTGTCTCTGCCCCCATCTTCAACCATATTGTGTCTTTTGGTGGCGGCC	600
QY	632	TCACCTCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGACGCGGGATGTCTCCACAG	691
D5	601	TCACCTCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGACGCGGGATGTCTCCACAG	660
QY	692	CAGGTACTGACGCCCTTGGAGGGCGAAGCTCTGTATGACAGACCTGACCTCTGACGTGGCC	751
D5	661	CAGGTACTGACGCCCTTGGAGGGCGAAGCTCTGTATGACAGACCTGACCTCTGACGTGGCC	720
QY	752	GGAACTCCCGGAAAGGCTTACCAGAAAGCTTTCTCTGCCAGGTTGACCAAGTGGAA	811
D5	721	GGAACTCCCGGAAAGGCTTACCAGAAAGCTTTCTCTGCCAGGTTGACCAAGTGGAA	780
QY	812	GTGGAATATGTACCATGGCTTCTTCCGGAAGGAGACATTTCTTAATGATCTCTGACC	871
D5	781	GTGGAATATGTACCATGGCTTCTTCCGGAAGGAGACATTTCTTAATGATCTCTGACC	840
QY	872	TTGGTGTGTGAGATCAGAACCGCACTACTGCAACATGGGCCAMCTCAGTACGCCAMCTY	931
D5	841	TTGGTGTGTGAGATCAGAACCGCACTACTGCAACATGGGCCAMCTCAGTACGCCAMCTY	900
QY	932	CCCGCAGGGGCGCTTGAGGAGCCCAAGCAATACAGCAACCATCAGCAGGCGCTTAGCCTGCA	991
D5	901	CCCGCAGGGGCGCTTGAGGAGCCCAAGCAATACAGCAACCATCAGCAGGCGCTTAGCCTGCA	960
QY	992	CTCCAGGCTCTTCTTTGAAACCCAGGCTGTGAGCACACTCTGTCCTCATCGACGCTCTGC	1051
D5	961	CTCCAGGCTCTTCTTTGAAACCCAGGCTGTGAGCACACTCTGTCCTCATCGACGCTCTGC	1020
QY	1052	CCCTCTGCTCCCTCATCAGGACCAACCCCGGGGATGTGTGCTCTGTCCTGATCAGCCAGCA	1111
D5	1021	CCCTCTGCTCCCTCATCAGGACCAACCCCGGGGATGTGTGCTCTGTCCTGATCAGCCAGCA	1080
QY	1112	TTGCCCTCTAGCTCTGGGTTGGGCTTGGGGCCAAAGTCTCAGGGGGCTCTTAGGAGTTGGG	1171
D5	1081	TTGCCCTCTAGCTCTGGGTTGGGCTTGGGGCCAAAGTCTCAGGGGGCTCTTAGGAGTTGGG	1140

RESULT 6

RESOLI 8
US-10-230-338-39

US-10-230-338-39
: Sequence 39, Application US/10230338

; Sequence 39, Application US/102
: Publication No. US20030044934A1

; Publication No. US20
; GENERAL INFORMATION:

ADDITIONAL INFORMATION: Baker Kevin D

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Chri

; APPLICANT: Grimaldi, J. Ch
: APPLICANT: Gurney. Austin

APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria

APPLICANT: Stephen Jean-Philippe

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

REF ID: A66666
TITLE OF INVENTION: SECRETED AND TRANSMEM

; TITLE OF INVENTION: SECRETED AND INFORMATION
; TITLE OF INVENTION: ACIDS ENCODING THE S; TITLE OF INVENTION: ACIDS ENCODING
: FILE REFERENCE: P3530P1C92

FILE REFERENCE: P3530PIC92
CURRENT APPLICATION NUMBER: US/10/230

;; CURRENT APPLICATION NUMBER: US/10/23
: CURRENT FILING DATE: 2002-08-28

; CURRENT FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-230-338-39

Query Match          97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAAGGCTGGAGTCTGTAGTTGTTCTGCTGCGCAGGCTCCACTGAGGGGAAC 91
DB 1 ACCACAGAGGCTGGAGTCTGTAGTTGTTCTGCTGCGCAGGCTCCACTGAGGGGAAC 60

QY 92 GGGGACCTGTCTGAAGAGAAGATGCCCTGTGTGACACTTACCTGCTCTCTTCTGCTC 151
DB 61 GGGGACCTGTCTGAAGAGAAGATGCCCTGTGTGACACTTACCTGCTCTCTTCTGCTC 120

QY 152 TCAGGCTACTCCATGCGCACTCAATCACCGGTCCACACAGTGAATGCTTGGACGG 211
DB 121 TCAGGCTACTCCATGCGCACTCAATCACCGGTCCACACAGTGAATGCTTGGACGG 180

QY 212 GGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 271
DB 181 GGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 240

QY 272 TGTGAGAGAGCTATTGGCGTGCATGCAAGTCTCTTTAAACAGTGGGTGAGCAG 331
DB 241 TGTGAGAGAGCTATTGGCGTGCATGCAAGTCTCTTTAAACAGTGGGTGAGCAG 300

QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAATCAGAAACACCGACGTTCACTGTG 391
DB 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAATCAGAAACACCGACGTTCACTGTG 360

QY 392 ACCATGGAGGATCTCATGAAGATGATGCTGACACTTACTGTTGGAATTGAGAAACT 451
DB 361 ACCATGGAGGATCTCATGAAGATGATGCTGACACTTACTGTTGGAATTGAGAAACT 420

QY 452 GGAATGACCTTGGGGTTCACAGTTCAAGTGAACCATTCAGCCAGCAGCAGTCAACCCAGAA 511
DB 421 GGAATGACCTTGGGGTTCACAGTTCAAGTGAACCATTCAGCCAGCAGCAGTCAACCCAGAA 480

QY 512 GAAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGACACAGGCAACAGCTCCTG 571
DB 481 GAAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGACACAGGCAACAGCTCCTG 540

QY 572 AAGCTCAGTGTCTCTGCGCCCTCATCTTCCACATATTCTGTTGTTGTTGTTGTTGTTG 631
DB 541 AAGCTCAGTGTCTCTGCGCCCTCATCTTCCACATATTCTGTTGTTGTTGTTGTTGTTG 600

QY 632 TCACCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCCGGATGTCCCCAGAG 691
DB 601 TCACCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCCGGATGTCCCCAGAG 660

QY 692 CAGGTACTGAGCCCTGGAGGGGACCTCTGCTATGACAGACTGACCTGACCTGAGCTGGCC 751
DB 661 CAGGTACTGAGCCCTGGAGGGGACCTCTGCTATGACAGACTGACCTGACCTGAGCTGGCC 720

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QY 752 GGAACCTCCCGCGAAGGCTACCAAGAGCTTTCTCTGCCAGGTTGACCAAGTGGAA 811
DB 721 GGAACCTCCCGCGAAGGCTACCAAGAGCTTTCTCTGCCAGGTTGACCAAGTGGAA 780

QY 812 GTGGAATATGTACCATGCTCTCTTCCGCAAGGAGGACATTTCTATGATCTCTGACC 871
DB 781 GTGGAATATGTACCATGCTCTCTTCCGCAAGGAGGACATTTCTATGATCTCTGACC 840

QY 872 TTGGGTGCTGAGGATCAGGAACCGACTACTGCAACATGGGCAMCTCAGTAGCCAMT 931
DB 841 TTGGGTGCTGAGGATCAGGAACCGACTACTGCAACATGGGCACCTCAGTAGCCACCTC 900

QY 932 CCGGAGGAGGCTCTGAGGAGCCACGGAATACAGCAATCAGCAGGCTTTAGCCTGCA 991
DB 901 CCGGAGGAGGCTCTGAGGAGCCACGGAATACAGCAATCAGCAGGCTTTAGCCTGCA 960

QY 992 CTCAGGCTCTCTTCTTGGACCCAGGCTGTGAGCACACTCTCTGCTCATCGACCTGTC 1051
DB 961 CTCAGGCTCTCTTCTTGGACCCAGGCTGTGAGCACACTCTCTGCTCATCGACCTGTC 1020

QY 1052 CCGCTGCTCCCTCATCAGGACCAACCGGGGAGCTGCTGCTCTCTGCTGATCAGCAGCA 1111
DB 1021 CCGCTGCTCCCTCATCAGGACCAACCGGGGAGCTGCTGCTCTCTGCTGATCAGCAGCA 1080

QY 1112 TTGCCCCAGCTGCTGGTTGGGCTTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTGGG 1171
DB 1081 TTGCCCCAGCTGCTGGTTGGGCTTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTGGG 1140

QY 1172 TTTTCTAAACGTCCTCTCTCT - CTACATAGTTGAGGAGGGGCTTAGGGATATGCTCTGG 1230
DB 1141 TTTTCTAAACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

QY 1231 GCGTTTCATGGAATGATGAAGATGATTAAGAAATGTTATCATTTATCATGAAG 1290
DB 1201 GCGTTTCATGGAATGATGAAGATGATTAAGAAATGTTATCATTTATCATGAAG 1260

QY 1291 TACCATTATCAATACCAATGAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1350
DB 1261 TACCATTATCAATACCAATGAACTTTATTTATTTGCTTACCAATGTTATGGGCTGAAT 1320

QY 1351 AATGGCCCCAAGATATCTGTGCTCTTAATCTCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
DB 1321 AATGGCCCCAAGATATCTGTGCTCTTAATCTCTCAGAACTTGTGACTGTTACCTTCTGTG 1380

QY 1411 GCAGAAAGGACAGTGCAGATGATTAAGTAAAGTTAAGGACTTTTGAATAGAGAGGTTATCT 1470
DB 1381 GCAGAAAGGACAGTGCAGATGATTAAGTAAAGTTAAGGACTTTTGAATAGAGAGGTTATCT 1440

QY 1471 TGCTGATTCAGGTGGGCCCCAAATATACCAAGGGTCTCTCATAAGAAAGAGGCCAGAA 1530
DB 1441 TGCTGATTCAGGTGGGCCCCAAATATACCAAGGGTCTCTCATAAGAAAGAGGCCAGAA 1500

QY 1531 GGTCAAGAGGTAGAGCAAAAGTGTGATGAAGTGGAGCTGGGGTGTGACCTGAGCAGGG 1590
DB 1501 GGTCAAGAGGTAGAGCAAAAGTGTGATGAAGTGGAGCTGGGGTGTGACCTGAGCAGGG 1560

QY 1591 GCCATGAATCCGCGAGCTTCCAGATGCCAGAAAGGAAAGGAATGGAATTCCTCTGCTCTGG 1650
DB 1561 GCCATGAATCCGCGAGCTTCCAGATGCCAGAAAGGAAAGGAATGGAATTCCTCTGCTCTGG 1620

QY 1651 AGCTTCCAAAGAAACAGCCCTGCGCCAGCTTGAAGTGTGAGCCCATGAACTGATCTT 1710
DB 1621 AGCTTCCAAAGAAACAGCCCTGCGCCAGCTTGAAGTGTGAGCCCATGAACTGATCTT 1680

QY 1711 GAGCTCTCTGGGCTCCAGAAATGCAAGGAAATAAATTTGTTGTTTATGAAAAAAA 1770
DB 1681 GAGCTCTCTGGGCTCCAGAAATGCAAGGAAATAAATTTGTTGTTTATGAAAAAAA 1740

QY 1771 AAAAAAATAAAAAA 1786
DB 1741 AAAAAAATAAAAAA 1756

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RESULT 7
US-10-218-631-39
; Sequence 39, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-631-39
Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAGCGTGGAGTCTGTAGTTTCTGCTGCCAGGCTCCACTGAGGGGAA 91
Db 1 ACCAGCAGAGCGTGGAGTCTGTAGTTTCTGCTGCCAGGCTCCACTGAGGGGAA 60
QY 92 GGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTCTGCTC 151
Db 61 GGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTCTGCTC 120
QY 152 TCAGGCTACTCCATTGCCACTCAATCACCAGTCCAAACAGTGAATGGCTTGGAGCG 211
Db 121 TCAGGCTACTCCATTGCCACTCAATCACCAGTCCAAACAGTGAATGGCTTGGAGCG 180
QY 212 GGCCTCTTGAACCGTCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGG 271
Db 181 GGCCTCTTGAACCGTCACTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGG 240
QY 272 TGTGAGGAGCTATTGGCGTGAATGCAAGATCCTTGTATTAACACAGTGGGTGAGCAG 331
Db 241 TGTGAGGAGCTATTGGCGTGAATGCAAGATCCTTGTATTAACACAGTGGGTGAGCAG 300
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332 GAGGTGAAGGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACGTTCACTGTG 391
301 GAGGTGAAGGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCGACGTTCACTGTG 360
392 ACCATGAGGATCTCATGAAAAATGATGCTGACACTTACTTGGTGTGAAATGAGAAACT 451
361 ACCATGAGGATCTCATGAAAAATGATGCTGACACTTACTTGGTGTGAAATGAGAAACT 420
452 GGAATGACCTTGGGGTCAAGTTCAAGTGACCAATGACCCAGCAGCAGCAGCAAGCTCTG 511
421 GGAATGACCTTGGGGTCAAGTTCAAGTGACCAATGACCCAGCAGCAGCAGCAAGCTCTG 480
512 GAAACTAGCAGCTCCCAACTCTGACCGGCAACACTTTGACACACAGGCAAGCTCTG 571
481 GAAACTAGCAGCTCCCAACTCTGACCGGCAACACTTTGACACACAGGCAAGCTCTG 540
572 AAGCTCAGTGTCTCTGCGCCCTCATCTTCCACATATTTKTYGTCTTTTGGTGGCGGCC 631
541 AAGCTCAGTGTCTCTGCGCCCTCATCTTCCACATATTTGCTGCTCTTTTGGTGGCGGCC 600
632 TCACCTCTTGGCTTGGAGGATGATGAAGTACACAGAGAAAGCAGCGGGATGTCCTCAGAG 691
601 TCACCTCTTGGCTTGGAGGATGATGAAGTACACAGAGAAAGCAGCGGGATGTCCTCAGAG 660
692 CAGTACTGACGCGCCCTGGAGGGGCACTCTGCTATGACGACCTGACCTCAGCTGAGTGC 751
661 CAGTACTGACGCGCCCTGGAGGGGCACTCTGCTATGACGACCTGACCTCAGCTGAGTGC 720
752 GGAACCTCCCGCGAAAGGCTTACACAGAAAGCTTCTCTGCCAGGTTGACAGGTGAA 811
721 GGAACCTCCCGCGAAAGGCTTACACAGAAAGCTTCTCTGCCAGGTTGACAGGTGAA 780
812 GTGGAATATGACCATGGCTTCTTGGCGGAGGAGCACTTCTCTATGATCTCTGACC 871
781 GTGGAATATGACCATGGCTTCTTGGCGGAGGAGCACTTCTCTATGATCTCTGACC 840
872 TTGGGTGCTGAGGATCAGAACCGGCTTCTGCAACTGGGCGCACTCAGTAGCCAMCTY 931
841 TTGGGTGCTGAGGATCAGAACCGGCTTCTGCAACTGGGCGCACTCAGTAGCCAMCTY 900
932 CCGCGCAGGGGCGCTGAGGAGGCCACGGAATACAGCAATACAGCAATACAGGAGGCTTAGCCTGCA 991
901 CCGCGCAGGGGCGCTGAGGAGGCCACGGAATACAGCAATACAGCAATACAGGAGGCTTAGCCTGCA 960
992 CTCAGGCTCTCTTCTTGACCCAGGCTGTGAGCAGCTCTGCTGCTCTATCGACCTCTGCG 1051
961 CTCAGGCTCTCTTCTTGACCCAGGCTGTGAGCAGCTCTGCTGCTCTATCGACCTCTGCG 1020
1052 CCGCTGCTCCCTCATCAGGACCAACCGGGGAGCTGTGCTCTCTGCTGATCAGCAGCA 1111
1021 CCGCTGCTCCCTCATCAGGACCAACCGGGGAGCTGTGCTCTCTGCTGATCAGCAGCA 1080
1112 TTGCCCCCTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG 1171
1081 TTGCCCCCTAGCTCTGGGTTGGGCTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG 1140
1172 TTCTCTAAAGTCCCTCTCTCT - CTACATAGTTGAGGAGGGGCTAGGAGATGCTCTGG 1230
1141 TTCTCTAAAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1200
1231 GGCTTTTCATGGGAATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAG 1290
1201 GGCTTTTCATGGGAATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAG 1260
1291 TACCATATCATATCAATGACCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1350
1261 TACCATATCATATCAATGACCTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1320
1351 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1410
1321 AATGGCCCCCAAGATATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1380
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QY 1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGACTTTGAGATAGAGAGGTTATTCT 1470
Db 1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGACTTTGAGATAGAGAGGTTATTCT 1440
QY 1471 TGCTGATTGAGTGGGCCCCCAATATACCAAGAGGTCCTCATAGAAAGAGGCGCAGAA 1530
Db 1441 TGCTGATTGAGTGGGCCCCCAATATATACCAAGAGGTCCTCATAGAAAGAGGCGCAGAA 1500
QY 1531 GGTCAAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGGTGTGACCTGAGCAGGG 1590
Db 1501 GGTCAAAGAGGTAGAGACAAAGTGTATGGAAGTGGACGTGGGTGTGACCTGAGCAGGG 1560
QY 1591 GCATGAAATGCGCGAGCTTCAGATGCCAGAAAGGAAGGAATGGATTCCCTCGCCTGG 1650
Db 1561 GCATGAAATGCGCGAGCTTCAGATGCCAGAAAGGAAGGAATGGATTCCCTCGCCTGG 1620
QY 1651 AGCTTCCAAAAGAACCCAGCCCTGCCACGCTTTGACTTGAGCCCATTTGAAACTGATCTT 1710
Db 1621 AGCTTCCAAAAGAACCCAGCCCTGCCACGCTTTGACTTGAGCCCATTTGAAACTGATCTT 1680
QY 1711 GAGCTCCTGGCTCCAGATTCAGAGGAGAAATTAATTTGTTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCCTGGCTCCAGATTCAGAGGAGAAATTAATTTGTTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAGAAAAA 1786
Db 1741 AAAAAAAGAAAAA 1756

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RESULT 8

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US-10-230-414-39
; Sequence 39, Application US/10230414
; Publication No. US2003005048A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39

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; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-414-39

Query Match      97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTCAGGGGAC 91
Db 1 ACCAGCAGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTCAGGGGAC 60
QY 92 GGGGACCTCTCTGAAGAGAGATGCCCTGTGACACTTACCTCTCTCTCTCTCTCTCT 151
Db 61 GGGGACCTCTCTGAAGAGAGATGCCCTGTGACACTTACCTCTCTCTCTCTCTCTCT 120
QY 152 TCAGGCTACTTCATTCGCCACTCAATATCACCGGTCCAAACAAACAGTGAATGGCTTGAGCGG 211
Db 121 TCAGGCTACTTCATTCGCCACTCAATATCACCGGTCCAAACAAACAGTGAATGGCTTGAGCGG 180
QY 212 GGTCTCTTGAACGCTGAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
Db 181 GGTCTCTTGAACGCTGAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240
QY 272 TGTGAGGAGCTATTGCGGTGACTGCAAGATCCTTGTATAACAGTGGGTGAGAGCAG 331
Db 241 TGTGAGGAGCTATTGCGGTGACTGCAAGATCCTTGTATAACAGTGGGTGAGAGCAG 300
QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAAGAAACCGCACCTTCACTGTG 391
Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACATCAAGAAACCGCACCTTCACTGTG 360
QY 392 ACCATGGAGGATCTCATGAAAACCTGATGCTGACACTTACTGGTGTGAATTTGAGAAACT 451
Db 361 ACCATGGAGGATCTCATGAAAACCTGATGCTGACACTTACTGGTGTGAATTTGAGAAACT 420
QY 452 GGAATGACCTTGGGCTCACAAGTTCAAGTACCATTGACCCAGACCACTCACCAGAA 511
Db 421 GGAATGACCTTGGGCTCACAAGTTCAAGTACCATTGACCCAGACCACTCACCAGAA 480
QY 512 GAACTAGACGCTCCCAACTCTGACCGGCGACCACTTGGACAAACAGSCAACAGCTCTG 571
Db 481 GAACTAGACGCTCCCAACTCTGACCGGCGACCACTTGGACAAACAGSCAACAGCTCTG 540
QY 572 AAGCTCAGTGTCTCTGCGCTCATCTTCAACATATTKYTGCTTTGGTGGCGGCC 631
Db 541 AAGCTCAGTGTCTCTGCGCTCATCTTCAACATATTKYTGCTTTGGTGGCGGCC 600
QY 632 TCACCTCTTGGCTTGGAGGATGATGAAGTACCAGAGAAAGCAGCGGAGTATCCCCAGAG 691
Db 601 TCACCTCTTGGCTTGGAGGATGATGAAGTACCAGAGAAAGCAGCGGAGTATCCCCAGAG 660
QY 692 CAGGTACTGACGCGCTGGAGGGGACCTCTGCTATGAGACCTGACCTGCACTGCGCTGCC 751
Db 661 CAGGTACTGACGCGCTGGAGGGGACCTCTGCTATGAGACCTGACCTGCACTGCGCTGCC 720
QY 752 GGAACCTCCCCGGAAGGCTTACCAAGAGCTTCTCTGCCCCAGGTTGACCAAGTGGAA 811
Db 721 GGAACCTCCCCGGAAGGCTTACCAAGAGCTTCTCTGCCCCAGGTTGACCAAGTGGAA 780
QY 812 GTGAATATGTACCATGGCTTCTTCCGAGAGGACATTTCTCTATGATCTGTACC 871
Db 781 GTGAATATGTACCATGGCTTCTTCCGAGAGGACATTTCTCTATGATCTGTACC 840
QY 872 TTGGGTGCTGAGGATCAGGAACCGACCTACTGGAACATGGCGCCAMCTCAGTACCCACTY 931
Db 841 TTGGGTGCTGAGGATCAGGAACCGACCTACTGGAACATGGCGCCAMCTCAGTACCCACTC 900
QY 932 CCCGGCAGGGGCTCTGAGGAGCCACGGAATACAGCAACCATCAGCAGGCTTACCTGTCA 991
Db 901 CCCGGCAGGGGCTCTGAGGAGCCACGGAATACAGCAACCATCAGCAGGCTTACCTGTCA 960

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QY 992 CTCAGGCTCTCTTGGACCCAGGCTGTGAGCACATCTCTGCTCATGACCGTCTGC 1051
Db 961 CTCAGGCTCTCTTGGACCCAGGCTGTGAGCACATCTCTGCTCATGACCGTCTGC 1020
QY 1052 CCCTGCTCCCTCATCAGGACCAACCCGGGACCTGCTGCTCTGCTGATCAGCCAGCA 1111
Db 1021 CCCTGCTCCCTCATCAGGACCAACCCGGGACCTGCTGCTCTGCTGATCAGCCAGCA 1080
QY 1112 TTGCCCCAGCTCTGGGTGGGCTTGGGGCCAGGCTCTAGGGGGCTTCTAGAGTTGGG 1171
Db 1081 TTGCCCCAGCTCTGGGTGGGCTTGGGGCCAGGCTCTAGGGGGCTTCTAGAGTTGGG 1140
QY 1172 TTTTCTAAACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
Db 1141 TTTTCTAAACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1231 GCTTTTCATGGGAATGATGAAGATGATATGAGAAATGTTATCATTTATCATGAAG 1290
Db 1201 GCTTTTCATGGGAATGATGAAGATGATATGAGAAATGTTATCATTTATCATGAAG 1260
QY 1291 TACCATTATCATAATACATGAACCTTTATTTATTTGCTCTACACATGTTATGGGCTGAAT 1350
Db 1261 TACCATTATCATAATACATGAACCTTTATTTATTTGCTCTACACATGTTATGGGCTGAAT 1320
QY 1351 AATGGCCCCAAGATATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1410
Db 1321 AATGGCCCCAAGATATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
QY 1411 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGAGTTATTTCT 1470
Db 1381 GCAGAAAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATAGAGAGTTATTTCT 1440
QY 1471 TGCTGATTCAGTGGGCCCCAAATATACACACAGGCTCTCATAGAAAGAGCCAGAA 1530
Db 1441 TGCTGATTCAGTGGGCCCCAAATATACACACAGGCTCTCATAGAAAGAGCCAGAA 1500
QY 1531 GGTCAAAGAGGTAGACACAAAGTATGATGGAAGTGGAGCTGGGTGTGACGTGAGCAGGG 1590
Db 1501 GGTCAAAGAGGTAGACACAAAGTATGATGGAAGTGGAGCTGGGTGTGACGTGAGCAGGG 1560
QY 1591 GCATGATTCGCGAGCTTCAATGTCAGAGAAAGGAAAGAAATGGAATTCCTGCTCTGG 1650
Db 1561 GCATGATTCGCGAGCTTCAATGTCAGAGAAAGGAAAGAAATGGAATTCCTGCTCTGG 1620
QY 1651 AGCTTCCAAAGAAACCGCCCTGCCACGCTTGAATGAGCCCATTTGAACTGATCTT 1710
Db 1621 AGCTTCCAAAGAAACCGCCCTGCCACGCTTGAATGAGCCCATTTGAACTGATCTT 1680
QY 1711 GAGCTCTGCTCCAGATTCAGAGGAAATGAAATTTGTTGTTGTTTAAATGAAAAAAA 1770
Db 1681 GAGCTCTGCTCCAGATTCAGAGGAAATGAAATTTGTTGTTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAATAAAAAA 1786
Db 1741 AAAAAAATAAAAAA 1756

RESULT 9

US-10-216-159A-39
; Sequence 39, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-159A-39

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCACAGAGCTGGGAGTCTGTAGTTTCTCTGCTGCAGCTCCACTGAGGGAAC 91
Db 1 ACCACAGAGCTGGGAGTCTGTAGTTTCTCTGCTGCAGCTCCACTGAGGGAAC 60
QY 92 GGGGACCTGTCTGAAGAGAGAGTCCCTCTGTGACACTCTACCTGCTCTCTTCTGCTC 151
Db 61 GGGGACCTGTCTGAAGAGAGAGTCCCTCTGTGACACTCTACCTGCTCTCTTCTGCTC 120
QY 152 TCAGGCTACTCCATGGCCACTCAANTCACCGTCCACACAGTGAATGCTTGGAGCGG 211
Db 121 TCAGGCTACTCCATGGCCACTCAANTCACCGTCCACACAGTGAATGCTTGGAGCGG 180
QY 212 GGTCTCTTGGCCGTGAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 271
Db 181 GGTCTCTTGGCCGTGAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGTGG 240
QY 272 TGTCGAGGAGTATTGGCGTGAATCAAGTCTCTTAAACCACTGGGTGAGAGCAG 331
Db 241 TGTCGAGGAGTATTGGCGTGAATCAAGTCTCTTAAACCACTGGGTGAGAGCAG 300
QY 332 GAGGTGAAGAGGAGCCGGGTGTCCATCAAGGACAATCAGAAAAACCGACGTTCACTGTG 391
Db 301 GAGGTGAAGAGGAGCCGGGTGTCCATCAAGGACAATCAGAAAAACCGACGTTCACTGTG 360
QY 392 ACCATGGAGGATCTCATGAATACTGATGCTGACACTTACTGCTGTGGAATGGAATACT 451
Db 361 ACCATGGAGGATCTCATGAATACTGATGCTGACACTTACTGCTGTGGAATGGAATACT 420
QY 452 GGAATGACCTTGGGGTCAAGTTCAGGTCACCAATGACCCAGCAGCAGTCAACCCAGAA 511
Db 421 GGAATGACCTTGGGGTCAAGTTCAGGTCACCAATGACCCAGCAGCAGTCAACCCAGAA 480
QY 512 GAACTAGCAGTCCCACTCTGACCGGCCACCACTTGGACACAGGACAGGCTCTG 571
Db 481 GAACTAGCAGTCCCACTCTGACCGGCCACCACTTGGACACAGGACAGGCTCTG 540

QY 572 AAGCTCAGTGTCTCTCTGCCCCCTCATCTTCAACAATATKYTGTCCTTTGGTGGCCCC 631
DB 541 AAGCTCAGTGTCTCTCTGCCCCCTCATCTTCAACAATATGCTGCTCTTTGGTGGCCCC 600
QY 632 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGCAGAAAGCAGCGGATGTCCCCAGAG 691
DB 601 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGCAGAAAGCAGCGGATGTCCCCAGAG 660
QY 692 CAGGTACTGACCCCTCGAGGCGCACTCTCTATGACAGCCTGACCCCTGACAGTGGCC 751
DB 661 CAGGTACTGACCCCTCGAGGCGCACTCTCTATGACAGCCTGACCCCTGACAGTGGCC 720
QY 752 GGAACCTCCCGGAAAGCTACCAAGAGCTTCTCTGCGCAGGTGACCAAGTGGAA 811
DB 721 GGAACCTCCCGGAAAGCTACCAAGAGCTTCTCTGCGCAGGTGACCAAGTGGAA 780
QY 812 GTGGAATATGTCAACATGGCTTCTTGGCGAAGGAGACATTTCTATGCACTCTGACC 871
DB 781 GTGGAATATGTCAACATGGCTTCTTGGCGAAGGAGACATTTCTATGCACTCTGACC 840
QY 872 TTGGGTGTGAGGATCAGGAACCGACCTACTGCAACATGGGCCAMCTCAGTAGCCAMCTY 931
DB 841 TTGGGTGTGAGGATCAGGAACCGACCTACTGCAACATGGGCCACCTCAGTAGCCACCTC 900
QY 932 CCGGCGAGGGGCGCTGAGGAGCCACCGAATACAGCACCATCAGCAGGCCCTTAGCCGTGCA 991
DB 901 CCGGCGAGGGGCGCTGAGGAGCCACCGAATACAGCACCATCAGCAGGCCCTTAGCCGTGCA 960
QY 992 CTCAGGCTCTCTTTGAGCCCGCAGGCTGTGAGCACACTCTGCTCATGCAAGCTGTC 1051
DB 961 CTCAGGCTCTCTTTGAGCCCGCAGGCTGTGAGCACACTCTGCTCATGCAAGCTGTC 1020
QY 1052 CCCCTGCTCCCTCATCAGGACCAACCGGGGACTGTGCTCTGCTGATCAGCAGCA 1111
DB 1021 CCCCTGCTCCCTCATCAGGACCAACCGGGGACTGTGCTCTGCTGATCAGCAGCA 1080
QY 1112 TTGCCCTTAGCTCTGGTGTGGCTTGGGCGCAAGTCTCAGGGGCTCTTAGGAGTTGGGG 1171
DB 1081 TTGCCCTTAGCTCTGGTGTGGCTTGGGCGCAAGTCTCAGGGGCTCTTAGGAGTTGGGG 1140
QY 1172 TTTTCTAAACCTCCCTCTCT-CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230
DB 1141 TTTTCTAAACCTCCCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1200
QY 1231 GCGTTTCAATGGAATGATGAAGATGATAAATGAGAAAAATGTTATCATTTATCATGAAG 1290
DB 1201 GCGTTTCAATGGAATGATGAAGATGATAAATGAGAAAAATGTTATCATTTATCATGAAG 1260
QY 1291 TACATTTATCATATACATGAACCTTTATTTATGCTTACCATGTTATGGCTGAAT 1350
DB 1261 TACATTTATCATATACATGAACCTTTATTTATGCTTACCATGTTATGGCTGAAT 1320
QY 1351 AATGGCCCCCAAGATATCTGTCTTAATCTCAGAACTTTGACTGTTACCTCTGTG 1410
DB 1321 AATGGCCCCCAAGATATCTGTCTTAATCTCAGAACTTTGACTGTTACCTCTGTG 1380
QY 1411 GCAGAAAGGGACATGAGATGATGAAGTTAAGGACTTTGAGATAGAGATTTATCT 1470
DB 1381 GCAGAAAGGGACATGAGATGATGAAGTTAAGGACTTTGAGATAGAGATTTATCT 1440
QY 1471 TGCTGATTTCAGGTGGGCCCAATATACACAGGGTCTCTATAGAAAGAGGCCAGAA 1530
DB 1441 TGCTGATTTCAGGTGGGCCCAATATACACAGGGTCTCTATAGAAAGAGGCCAGAA 1500
QY 1531 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTGAGCTGAGCAGGG 1590
DB 1501 GGTCAAGAGGTAGAGACAAAGTATGATGGAAGTGGACGTGGGTGTGAGCTGAGCAGGG 1560
QY 1591 GCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGGAATGATTCCTCTGCTGG 1650
DB 1561 GCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGGAATGATTCCTCTGCTGG 1620
QY 1651 AGCCTCCAAAAGAAACCAGCGCTTGCACCGCTTGACTTGAGGCCATTTGAAACTGATCTT 1710

DB 1621 AGCCTCCAAAAGAAACCAGCGCTTGCACCGCTTGACTTGAGCCCATTTGAACTGATCTT 1680
QY 1711 GAGCTCTGCGCTCCCAAGATTCAGAGAGATAAATTTGTTGTTTAAATGAAAAAAA 1770
DB 1681 GAGCTCTGCGCTCCCAAGATTCAGAGAGATAAATTTGTTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAATAAAAAA 1786
DB 1741 AAAAAAATAAAAAA 1756
RESULT 10
US-10-218-849-39
; Sequence 39, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/218,849
; Prior Application: 2002-08-12
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 39
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-218-849-39
Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
QY 32 ACCAGCAGAGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAAC 91
DB 1 ACCAGCAGAGCTGGGAGTCTGTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAAC 60
QY 92 GGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTCTTCTGGCTC 151
DB 61 GGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTCTACCTGCTCTCTCTTCTGGCTC 120
QY 152 TCAGGCTACTCCATTGCGCACTCAAAATCAACCGGTCCAAACAGTGAATGGCTTGGAGCG 211
DB 121 TCAGGCTACTCCATTGCGCACTCAAAATCAACCGGTCCAAACAGTGAATGGCTTGGAGCG 180
QY 212 GGTCTCTTGAAGGTCAGTGTGTTTACAGATCAGGCTGGGAGCTTCTTGAAGTGGTG 271
DB 181 GGTCTCTTGAAGGTCAGTGTGTTTACAGATCAGGCTGGGAGCTTCTTGAAGTGGTG 240
QY 272 TGTGAGAGGATTTTGGCGTGAAGTCTTGTAAACCCAGTGGGTGAGAGCAG 331
DB 241 TGTGAGAGGATTTTGGCGTGAAGTCTTGTAAACCCAGTGGGTGAGAGCAG 300
QY 332 GAGGTGAAGGGGACCGGTGTCATCAAGACATCAGAAACCCGACGTTCACTGTG 391
DB 301 GAGGTGAAGGGGACCGGTGTCATCAAGACATCAGAAACCCGACGTTCACTGTG 360
QY 392 ACCATGGAGGATCTCATGAAACCTGATGCTGACACTTACTGTTGGAATTTGAAAAACT 451
DB 361 ACCATGGAGGATCTCATGAAACCTGATGCTGACACTTACTGTTGGAATTTGAAAAACT 420

QY 452 GGAATGACCTTGGGTGTCAGTTCAAGTGAACCATTTGACCCAGCACCAGCTACCCAGAA 511
DB 421 GGAATGACCTTGGGTGTCAGTTCAAGTGAACCATTTGACCCAGCACCAGCTACCCAGAA 480
QY 512 GAACTAGCAGCTCCCACTCTGACCGGCGCACCACTTGGAACAAGGACCAAGCTCTG 571
DB 481 GAACTAGCAGCTCCCACTCTGACCGGCGCACCACTTGGAACAAGGACCAAGCTCTG 540
QY 572 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAATATTKYGTGTTTGTGGCGGCC 631
DB 541 AAGCTCAGTGTCTCTGCGCCCTCATCTTCAATATTKYGTGTTTGTGGCGGCC 600
QY 632 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGAAAGCAGCGGGATGTCCCCAGAG 691
DB 601 TCACTCTTGGCTTGGAGGATGATGAAGTACACAGAAAGCAGCGGGATGTCCCCAGAG 660
QY 692 CAGGTACTGACGCCCTTGGAGGCGACCTCTGTATGCAACCTGACCTGAGCTGGCC 751
DB 661 CAGGTACTGACGCCCTTGGAGGCGACCTCTGTATGCAACCTGACCTGAGCTGGCC 720
QY 752 GGAACCTCCCGGAAGGCTACCAAGAGCTTCTCTGCCAGGTTGACCAAGTGGAA 811
DB 721 GGAACCTCCCGGAAGGCTACCAAGAGCTTCTCTGCCAGGTTGACCAAGTGGAA 780
QY 812 GTGGAATATGTCACCATGGCTTCTTCCGGAAGGAGACATTTCTTATGCACTCTGACC 871
DB 781 GTGGAATATGTCACCATGGCTTCTTCCGGAAGGAGACATTTCTTATGCACTCTGACC 840
QY 872 TTGGGTCTGAGGATCAGAACCGAAGCTTCTGAAACATGAGGCGCCAMCTCAGTAGCCATY 931
DB 841 TTGGGTCTGAGGATCAGAACCGAAGCTTCTGAAACATGAGGCGCCAMCTCAGTAGCCATY 900
QY 932 CCGGGCAGGGGCCCTGAGGAGCCACGGAATACAGACCATCAGAGGCCCTTACGCTGCA 991
DB 901 CCGGGCAGGGGCCCTGAGGAGCCACGGAATACAGACCATCAGAGGCCCTTACGCTGCA 960
QY 992 CTCAGGCTCTCTTGGACCCAGGCTGTGAGACACTCTGCTCATCGACCTGTGC 1051
DB 961 CTCAGGCTCTCTTGGACCCAGGCTGTGAGACACTCTGCTCATCGACCTGTGC 1020
QY 1052 CCCCTGCTCCCTCATCAGACCAACCCGGGAGCTGGTCTCTGCTGATCAGCCAGCA 1111
DB 1021 CCCCTGCTCCCTCATCAGACCAACCCGGGAGCTGGTCTCTGCTGATCAGCCAGCA 1080
QY 1112 TTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGGAGTTGGG 1171
DB 1081 TTGCCCCCTAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGGAGTTGGG 1140
QY 1172 TTTTCTAAAGCTCCCTCTCT - CTACATAGTTGAGAGGGGCTAGGATATGCTCTGG 1230
DB 1141 TTTTCTAAAGCTCCCTCTCTCTCTACATAGTTGAGAGGGGCTAGGATATGCTCTGG 1200
QY 1231 GGGTTTCTAGGAAATGATGAAGATGATAATGAGAAATGTTATCATTTATCATGAAG 1290
DB 1201 GGGTTTCTAGGAAATGATGAAGATGATAATGAGAAATGTTATCATTTATCATGAAG 1260
QY 1291 TACCATATCATATAACAAAGCTTTATTTATTTGCTTACCAATGTTATGGCTGAAT 1350
DB 1261 TACCATATCATATAACAAAGCTTTATTTATTTGCTTACCAATGTTATGGCTGAAT 1320
QY 1351 AATGGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1410
DB 1321 AATGGCCCCCAAGATATCTGTCTCTAATCTCAGAACTTGTGACTGTTACCTTCTGTG 1380
QY 1411 GCAGAAAGGGCAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1470
DB 1381 GCAGAAAGGGCAGTGCAGATGTATGTAAGTTAAGGACTTTGAGATAGAGAGTTATCT 1440
QY 1471 TGCTGATTCAGTGGGCCCAAAATATACCAACAGGGTCTCTATAAGAAAGAGCCAGAA 1530
DB 1441 TGCTGATTCAGTGGGCCCAAAATATACCAACAGGGTCTCTATAAGAAAGAGCCAGAA 1500
QY 1531 GGTCAAGAGGTAGACACAAAGTGTATGGAAGTGGACGTGGGTGTGACGTGACGAGG 1590

DB 1501 GGTCAAGAGGTAGAGACAAAGTGATGATGAAGTGGACGTGGGTGTGACGTGACGAGG 1560
QY 1591 GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGATGGATTCCCTGCGCTGG 1650
DB 1561 GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGAAAGATGGATTCCCTGCGCTGG 1620
QY 1651 AGCCTCCAAAAGAAACACAGCCCTGCCACGCTTGTACTTGAGCCCATTTGAAACTGATCTT 1710
DB 1621 AGCCTCCAAAAGAAACACAGCCCTGCCACGCTTGTACTTGAGCCCATTTGAAACTGATCTT 1680
QY 1711 GAGCTCTGGGCTCCAGAAATTCAGAGGAGATAAATTTGTGTGTTTAAATGAAAAAAA 1770
DB 1681 GAGCTCTGGGCTCCAGAAATTCAGAGGAGATAAATTTGTGTGTTTAAATGAAAAAAA 1740
QY 1771 AAAAAAAGAAAAA 1786
DB 1741 AAAAAAAGAAAAA 1756

RESULT 11
US-10-227-873-39
; Sequence 39, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC72
; CURRENT APPLICATION NUMBER: US/10/227,873
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR APPLICATION NUMBER: 60/146222
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; PRIOR FILING DATE: 1999-08-17
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; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

32 ACAGCAGAGAGGTGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGGAC 91
Db
1 ACAGCAGAGAGGTGGAGTCTGTAGTTTGTCTCTGCTGCCAGGCTCCACTGAGGGGAC 60
Qy
92 GGGGACCTGTCTCAAGAGAGAGATGCCCTGTCTGACACTCTTACCTGTCTCTTCTGGCTC 151
Db
61 GGGGACCTGTCTGAGAGAGAGATGCCCTGTCTGACACTCTTACCTGTCTCTTCTGGCTC 120
Qy
152 TCAGGCTACTCCATTCGCACTCAAAATCCGCTGCAACAGAGTGAATGGCTTGGAGCGG 211
Db
121 TCAGGCTACTCCATTCGCACTCAAAATCCGCTGCAACAGAGTGAATGGCTTGGAGCGG 180
Qy
212 GGCTCCTTGACCGTGAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
Db
181 GGCTCCTTGACCGTGAGTGTGTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240
Qy
272 TGTCCGAGAGCTATTTGGCGTGAATGCAAGATCCTTTTAAACCAAGTGGGTGAGAGCAG 331
Db
241 TGTCCGAGAGCTATTTGGCGTGAATGCAAGATCCTTTTAAACCAAGTGGGTGAGAGCAG 300
Qy
332 GAGTGAAGAGGACCGGTGTCCATCAAGAGCAATCAGAAACCGCAGTTCACCTGTG 391
Db
301 GAGTGAAGAGGACCGGTGTCCATCAAGAGCAATCAGAAACCGCAGTTCACCTGTG 360
Qy
392 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTTGGTGGAAATGAGAAACT 451
Db
361 ACCATGAGGATCTCATGAAACCTGATGCTGACACTTACTTGGTGGAAATGAGAAACT 420
Qy
452 GGAATGACCTTGGGGTCAAGTTCAAGTGAACATTGACCCAGCAACAGTCAACCAAGAA 511
Db
421 GGAATGACCTTGGGGTCAAGTTCAAGTGAACATTGACCCAGCAACAGTCAACCAAGAA 480
Qy
512 GAAACTAGCAGCTCCCAACTCTGACCGGACCACTTGGACACAGGCAAGTCTCTG 571
Db
481 GAAACTAGCAGCTCCCAACTCTGACCGGACCACTTGGACACAGGCAAGTCTCTG 540
Qy
572 AAGTCTAGTGTCTCTGCTCCCTCATCTTCAACATATKVTGYGTCTTTTGGTGGCGCC 631
Db
541 AAGTCTAGTGTCTCTGCTCCCTCATCTTCAACATATGCTGTCTTTTGGTGGCGCC 600
Qy
632 TCACCTTGGCTTGGAGATGATGAATACAGCAGAAAGCGCGGATGTCGCCAGAG 691
Db
601 TCACCTTGGCTTGGAGATGATGAATACAGCAGAAAGCGCGGATGTCGCCAGAG 660
Qy
692 CAGGTACTGACGCCCCCTGGAGGGGACCTCTGTATGACAGACCTGACCCCTGCAGCTGCC 751
Db
661 CAGGTACTGACGCCCCCTGGAGGGGACCTCTGTATGACAGACCTGACCCCTGCAGCTGCC 720
Qy
752 GGAACCTCCCGGAAAGGCTACACAGAGCTTTCTCTGCTGCCAGGTTGACAGGTGGAA 811
Db
721 GGAACCTCCCGGAAAGGCTACACAGAGCTTTCTCTGCTGCCAGGTTGACAGGTGGAA 780
Qy
812 GTGGAATATGACCATGCTCTCTTGGCGAGGAGGACATTTCTATGCAATCTCTGACC 871
Db
781 GTGGAATATGACCATGCTCTCTTGGCGAGGAGGACATTTCTATGCAATCTCTGACC 840
Qy
872 TTGGGTGTGAGGATCAGGAACCGACCTACTTGCACATGGGCCAMCTCAGTAGCCAMCTY 931
Db
841 TTGGGTGTGAGGATCAGGAACCGACCTACTTGCACATGGGCCACCTCAGTAGCCACCTC 900
Qy
932 CCGGAGGGGCGCTGAGAGCCGACGGAATACACACATCAGCAGCCCTTAGCTTGA 991
Db
901 CCGGAGGGGCGCTGAGAGCCGACGGAATACACACATCAGCAGCCCTTAGCTTGA 960
Qy
992 CTCAGGGCTCTTCTTGGACCCCGAGGCTGTGAGCAGCACTCTCTGCTCATCGACCGTCTGC 1051

961 CTCAGGCTCTTCTTGGACCCAGGCTGTGAGCACACTCTGCTCATCGACGCTGC 1020
Qy
1052 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1111
Db
1021 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGTGCTCTGCTGATCAGCCAGCA 1080
Qy
1112 TTGCCCTAGTCTCTGGGTGGGCTTGGGCCAAGTCTCAGGGGCTCTTAGAGTTGGGG 1171
Db
1081 TTGCCCTAGTCTCTGGGTGGGCTTGGGCCAAGTCTCAGGGGCTCTTAGAGTTGGGG 1140
Qy
1172 TTTTCTAAACGCTCCCTCTCT - CTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1230
Db
1141 TTTTCTAAACGCTCCCTCTCTCTACATAGTTGAGGAGGGGCTAGGATATGCTCTGG 1200
Qy
1231 GGTCTTCAATGGAATGATGAAGATGAATGAGAAAAATGTTATCAITATTATCATGAAG 1290
Db
1201 GGTCTTCAATGGAATGATGAAGATGAATGAGAAAAATGTTATCAITATTATCATGAAG 1260
Qy
1291 TACCAATTATCAATAFACAACTTTATTTATTTGCTTACCATATGTTATGGGCTGAAT 1350
Db
1261 TACCAATTATCAATAFACAACTTTATTTATTTGCTTACCATATGTTATGGGCTGAAT 1320
Qy
1351 AATGGCCCCCAAGATATCTGTCTTAATCCTCAGAACTTTGTGACTGTTACCTTCTGTG 1410
Db
1321 AATGGCCCCCAAGATATCTGTCTTAATCCTCAGAACTTTGTGACTGTTACCTTCTGTG 1380
Qy
1411 GCAGAAAGGACAGTGCAGATGTTATGTAAGTTAAGACTTTTGAGATAGAGAGTTATCT 1470
Db
1381 GCAGAAAGGACAGTGCAGATGTTATGTAAGTTAAGACTTTTGAGATAGAGAGTTATCT 1440
Qy
1471 TGCTGATTCAGGTGGGCCCCCAATATCACCAGAGGTCCTCATAGAAAGAGGCGCAGAA 1530
Db
1441 TGCTGATTCAGGTGGGCCCCCAATATCACCAGAGGTCCTCATAGAAAGAGGCGCAGAA 1500
Qy
1531 GGTCAAGAGAGGTAGAGACAAAGTGTATGTAAGTTAAGACTTTTGAGATAGAGAGTTATCT 1590
Db
1501 GGTCAAGAGAGGTAGAGACAAAGTGTATGTAAGTTAAGACTTTTGAGATAGAGAGTTATCT 1560
Qy
1591 GGCATGAATGCGCGACCTTTCAGATGCCAGAAAGGAAAGNATGGATCCCTCCCTGG 1650
Db
1561 GGCATGAATGCGCGACCTTTCAGATGCCAGAAAGGAAAGNATGGATCCCTCCCTGG 1620
Qy
1651 AGCCTCCAAAGAAACCCAGCCTGCCCGCTTGCATTTGAGCCCATGAAACTGATCTT 1710
Db
1621 AGCCTCCAAAGAAACCCAGCCTGCCCGCTTGCATTTGAGCCCATGAAACTGATCTT 1680
Qy
1711 GAGCTCTGGCTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAATGAAAAAAA 1770
Db
1681 GAGCTCTGGCTCCAGAAATTCAGAGAAATAAATTTGTGTTGTTTAAATGAAAAAAA 1740
Qy
1771 AAAAAAAGGAAAAA 1786
Db
1741 AAAAAAAGGAAAAA 1756

RESULT 12
US-10-227-883-39
; Sequence 39, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Stephanie
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3530PIC78
;; CURRENT APPLICATION NUMBER: US/10/227,883
;; CURRENT FILING DATE: 2002-08-26
;; PRIOR APPLICATION NUMBER: 10/119,480
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089905
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090691
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095318
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095916
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/096146
;; PRIOR FILING DATE: 1998-08-11
;; PRIOR APPLICATION NUMBER: 60/096791
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/097986
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: 60/098544
;; PRIOR FILING DATE: 1998-08-31
;; PRIOR APPLICATION NUMBER: 60/099596
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099598
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099816
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100038
;; PRIOR FILING DATE: 1998-09-11
;; PRIOR APPLICATION NUMBER: 60/100385
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
;; PRIOR FILING DATE: 1998-09-25
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/106178
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30
;; PRIOR APPLICATION NUMBER: 60/106905
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/108787
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21

[illegible]

Db 1501 GGTCAAGAGGTAGAGACAAAGTGATGATGGAAGTGGACGTGGGTGTCACGTGAGCAGGG 1560
 QY 1591 GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGGAAGAAATGCCCTGCTGG 1650
 Db 1561 GCCATGAATGCCGAGCCTTCAGATGCCAGAAAGGGAAGAAATGCCCTGCTGG 1620
 QY 1651 AGCCTCCAAAAGAAACCAAGCCCTGCCACGCTTGCATTTGAGCCCATTTGAAACTGATCTT 1710
 Db 1621 AGCCTCCAAAAGAAACCAAGCCCTGCCACGCTTGCATTTGAGCCCATTTGAAACTGATCTT 1680
 QY 1711 GAGCTCTGGCTCCAGAAATTCAGAGAGAAATTAATTTGTGTGTTTAAATGAAAAAAA 1770
 Db 1681 GAGCTCTGGCTCCAGAAATTCAGAGAGAAATTAATTTGTGTGTTTAAATGAAAAAAA 1740
 QY 1771 AAAAAAAAAAAAAA 1786
 Db 1741 AAAAAAAAAAAAAA 1756

RESULT 13
 US-10-219-076-39
 ; Sequence 39, Application US/10219076
 ; Publication No. US20030078379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C62
 ; CURRENT APPLICATION NUMBER: US/10/219,076
 ; PRIORITY FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIORITY FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIORITY FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIORITY FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIORITY FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIORITY FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIORITY FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIORITY FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIORITY FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIORITY FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIORITY FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 39
 ; LENGTH: 1837
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-219-076-39

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;
 QY 32 ACCAGCAGAGGCTGGGAGTCTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAGAC 91

Db 1 ACCAGCAGAGGCTGGGAGTCTAGTTTGTCTGCTGCCAGGCTCCACTGAGGGGAGAC 60
 QY 92 GGGGACCTGTCTGAAGAGAGATGCCCTGCTGACACTCTACCTGCTCTCTTCTGGCTC 151
 Db 61 GGGGACCTGTCTGAAGAGAGATGCCCTGCTGACACTCTACCTGCTCTCTTCTGGCTC 120
 QY 152 TCAGGCTACTCCATTGCCACTCAAAATCACCGGTCCAAACAAAGTGAATGGCTTGGAGCGG 211
 Db 121 TCAGGCTACTCCATTGCCACTCAAAATCACCGGTCCAAACAAAGTGAATGGCTTGGAGCGG 180
 QY 212 GGCCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 271
 Db 181 GGCCTCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGG 240
 QY 272 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACCAAGTGGGTGAGAGCAG 331
 Db 241 TGTGAGGAGCTATTTGGCGTGACTGCAAGATCCTTGTAAACCAAGTGGGTGAGAGCAG 300
 QY 332 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCCGACGTTCACTGTG 391
 Db 301 GAGGTGAAGAGGACCGGGTGTCCATCAAGGACAAATCAGAAAAACCCGACGTTCACTGTG 360
 QY 392 ACCATGGAGGATCTCATGAAATCTGATCTGACACTTACTGTGTGGAAATTCAGAAAACT 451
 Db 361 ACCATGGAGGATCTCATGAAATCTGATCTGACACTTACTGTGTGGAAATTCAGAAAACT 420
 QY 452 GGAATGACCTTTGGGGTTCACAGTTCAAGTGACCAATTCAGCCAGCACCACTCACCAGAA 511
 Db 421 GGAATGACCTTTGGGGTTCACAGTTCAAGTGACCAATTCAGCCAGCACCACTCACCAGAA 480
 QY 512 GAACTAGCAGCTCCCAACTCTGACCGCCACCACTTGGACCAAGCAGCAAGCTCCCTG 571
 Db 481 GAACTAGCAGCTCCCAACTCTGACCGCCACCACTTGGACCAAGCAGCAAGCTCCCTG 540
 QY 572 AAGCTCAGTGTCTCTGCTCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCCGCC 631
 Db 541 AAGCTCAGTGTCTCTGCTCCCTCATCTTCAACATATTKYTGCTTTTGGTGGCCGCC 600
 QY 632 TCATCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCTCCAGAG 691
 Db 601 TCATCTTGGCTTGGAGGATGATGAAGTACAGCAGAAAGCAGCGGGATGTCCTCCAGAG 660
 QY 692 CAGGTACTGCAGCCCTCGAGGGGACCTCTGCTATGAGACCTGACCCCTCAGCTGGCC 751
 Db 661 CAGGTACTGCAGCCCTCGAGGGGACCTCTGCTATGAGACCTGACCCCTCAGCTGGCC 720
 QY 752 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCCAGGTTGACAGGTGGAA 811
 Db 721 GGAACCTCCCGCGAAAGGCTACCAAGAGCTTCTCTGCCAGGTTGACAGGTGGAA 780
 QY 812 GTGGAATATGTCACCATGGCTTCCTTCCGAGGAGGACATTCCTATGCACTCTGACC 871
 Db 781 GTGGAATATGTCACCATGGCTTCCTTCCGAGGAGGACATTCCTATGCACTCTGACC 840
 QY 872 TTGGGTGTGAGGATCAGAAACCGACCTTACTGCAACATGGGCCAMCTCAGTAGCCACTY 931
 Db 841 TTGGGTGTGAGGATCAGAAACCGACCTTACTGCAACATGGGCCAMCTCAGTAGCCACTY 900
 QY 932 CCGGCGAGGGGCTTGGAGGAGCCAGGAATACAGCACCATCAGAGGCTTAGCTGCA 991
 Db 901 CCGGCGAGGGGCTTGGAGGAGCCAGGAATACAGCACCATCAGAGGCTTAGCTGCA 960
 QY 992 CTCAGAGGCTCTTCTTGGACCCAGGCTGTGAGACACTCTCTGCTCATCAGCCGTCTGC 1051
 Db 961 CTCAGAGGCTCTTCTTGGACCCAGGCTGTGAGACACTCTCTGCTCATCAGCCGTCTGC 1020
 QY 1052 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGCTGCTCTGCTGATCAGCAGCA 1111
 Db 1021 CCCCTGCTCCCTCATCAGGACCAACCCGGGAGCTGCTGCTCTGCTGATCAGCAGCA 1080
 QY 1112 TTGGCCCTAGCTCTGGGTGGGCTTGGGGCCAAAGTCTCAGGGGCTTCTAGAGTTGGG 1171

Db	1081	TTGCCCTAGCTCTGGGTTGGGCTTGGGGCCAAAGTCTCAGGGGGCTTCTAGGAGTTGGG	1140	/	PRIOR FILING DATE: 1997-10-17
Qy	1172	TTTTCTAAAGCTCCCTCTCTCT-CTACATAGTTGAGAGGGGGCTAGGATATGCTCTGG	1230	/	PRIOR APPLICATION NUMBER: 60/063549
Db	1141	TTTTCTAAAGCTCCCTCTCTCTCTACATAGTTGAGAGGGGGCTAGGATATGCTCTGG	1200	/	PRIOR FILING DATE: 1997-10-28
Qy	1231	GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATATTATTATCATGAAG	1290	/	PRIOR APPLICATION NUMBER: 60/064103
Db	1201	GGCTTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATATTATTATCATGAAG	1260	/	PRIOR FILING DATE: 1997-10-31
Qy	1291	TACCATTCATTAATCAATGAACCTTTTATTTATTCCTTACCATTCACATGTTATGGGCTGAAT	1350	/	PRIOR APPLICATION NUMBER: 60/069873
Db	1261	TACCATTCATTAATCAATGAACCTTTTATTTATTCCTTACCATTCACATGTTATGGGCTGAAT	1320	/	PRIOR FILING DATE: 1997-12-17
Qy	1351	AATGGCCCCCAAGATATCTGTCTCTATCTCTAATCTCTCAGAACTTGTCGACTTTACCTTCTGTG	1410	/	PRIOR APPLICATION NUMBER: 60/078910
Db	1321	AATGGCCCCCAAGATATCTGTCTCTAATCTCTCAGAACTTGTCGACTTTACCTTCTGTG	1380	/	PRIOR FILING DATE: 1998-03-20
Qy	1411	GCAGAAAGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATGAGAGGTTATCT	1470	/	PRIOR APPLICATION NUMBER: 60/079294
Db	1381	GCAGAAAGGACAGTGCAGATGTATGTAAAGTTAAGGACTTTGAGATGAGAGGTTATCT	1440	/	PRIOR FILING DATE: 1998-03-25
Qy	1471	TGCTGATTGAGTGGGCCCCCAATATATCACCACAAAGGCTCTCATAGAAAGAGGCCAGAA	1530	/	PRIOR APPLICATION NUMBER: 60/079656
Db	1441	TGCTGATTGAGTGGGCCCCCAATATATCACCACAAAGGCTCTCATAGAAAGAGGCCAGAA	1500	/	PRIOR FILING DATE: 1998-03-26
Qy	1531	GGTCAAGAGGTAGACAAAGTGTATGATGAAAGTGGACGTGGGTGTGACGTGAGCAGGG	1590	/	PRIOR APPLICATION NUMBER: 60/079728
Db	1501	GGTCAAGAGGTAGACAAAGTGTATGATGAAAGTGGACGTGGGTGTGACGTGAGCAGGG	1560	/	PRIOR FILING DATE: 1998-03-27
Qy	1591	GCCATGAATCCGAGCCTTCAGATGCCAGAAAGGGAAGGAATGGAATCCCTGCTCTGG	1650	/	PRIOR APPLICATION NUMBER: 60/081819
Db	1561	GCCATGAATCCGAGCCTTCAGATGCCAGAAAGGGAAGGAATGGAATCCCTGCTCTGG	1620	/	PRIOR FILING DATE: 1998-04-15
Qy	1651	AGCTCCAAAGAAACAGCCCTGCGCCAGCCCTTGACTTGAGCCCATTTGAACTGATCTT	1710	/	PRIOR APPLICATION NUMBER: 60/081955
Db	1621	AGCTCCAAAGAAACAGCCCTGCGCCAGCCCTTGACTTGAGCCCATTTGAACTGATCTT	1680	/	PRIOR FILING DATE: 1998-04-15
Qy	1711	GAGCTCTGCGCTCCAGAAATTCAGAGGAGAAATAATTTGTTCTTTTAAATGAAAAAAA	1770	/	PRIOR APPLICATION NUMBER: 60/082804
Db	1681	GAGCTCTGCGCTCCAGAAATTCAGAGGAGAAATAATTTGTTCTTTTAAATGAAAAAAA	1740	/	PRIOR FILING DATE: 1998-04-22
Qy	1771	AAAAAAAAAAAAAAAAA 1786		/	PRIOR APPLICATION NUMBER: 60/084441
Db	1741	AAAAAAAAAAAAAAAAA 1756		/	PRIOR FILING DATE: 1998-05-06

RESULT 14
US-10-230-434-39
; Sequence 39, Application US/10230434
; Publication No. US20030078380A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C82
; CURRENT APPLICATION NUMBER: US/10/230.434
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287

Db 541 AAGCTCAGTGTCTCTCTGCCCCCTCATCTTCAACCATATTCCTGCTGCTTTTGTGTGCGCCG 600
Qy 632 TCACTCTTGTGCTTGGAGGATGATGAAGTACCAGCAGAAAGCAGCGGGATGTCCCCAGAG 691
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Qy 692 CAGGTACTGACGCCCTTGAGGGCGACCTCTGTATGACAGCTGACCTGACGCTGCCC 751
Db 661 CAGGTACTGACGCCCTTGAGGGCGACCTCTGTATGACAGCTGACCTGACGCTGCCC 720
Qy 752 GGAACCTCCCGGAAAGGCTACCAAGAGCTTCTCTGCCCCAGGTTGACAGGTGGAA 811
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Qy 872 TTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGCCGACCTCAGTAGCCACCTY 931
Db 841 TTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGCCGACCTCAGTAGCCACCTC 900
Qy 932 CCGGCGAGGGGCGCTGAGGAGCCACGGGAATACAGCACCATCAGCAGGCGCTTAGCCTGCA 991
Db 901 CCGGCGAGGGGCGCTGAGGAGCCACGGGAATACAGCACCATCAGCAGGCGCTTAGCCTGCA 960
Qy 992 CTCAGGCTCTTCTTGGACCCAGGCTGTGACACACTCTGCTGCTCATCGACCGCTGCG 1051
Db 961 CTCAGGCTCTTCTTGGACCCAGGCTGTGACACACTCTGCTGCTCATCGACCGCTGCG 1020
Qy 1052 CCGCTGCTCCCTCATCAGGACCAACCCGGGGACTGTGCTCTGCTGCTGATCAGCCAGCA 1111
Db 1021 CCGCTGCTCCCTCATCAGGACCAACCCGGGGACTGTGCTCTGCTGCTGATCAGCCAGCA 1080
Qy 1112 TTGCCCCAGCTCTGGGTTGGGTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG 1171
Db 1081 TTGCCCCAGCTCTGGGTTGGGTTGGGCGCAAGTCTCAGGGGGCTTCTAGGAGTTGGG 1140
Qy 1172 TTTTCTAAAGTCCCTCTCT - CTACATAGTTGAGGAGGGGCTAGGGATATGCTCTGG 1230
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Db 1561 GCCATGATCCGAGCCTTCAGATGCCAGAAAGGAAAGAAATGGAATCCCTGCTGG 1620
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Db 1621 AGCCTCCAAAAGAAACCAAGCCCTGCCACGCTTCACTTGAGCCCATGAAACTGATCTT 1680

RESULT 15

US-10-219-003-39
; Sequence 39, Application US/10219003
; Publication No. US20030088063A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/079656
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; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24

Qy 1711 GAGTCTCGCTCCAGAAATTCAGGAGAAATTTGTGTTTAAATGAAAAA 1770
Db 1681 GAGTCTCGCTCCAGAAATTCAGGAGAAATTTGTGTTTAAATGAAAAA 1740
Qy 1771 AAAAAA 1786
Db 1741 AAAAAA 1756

; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090691
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/095302
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095318
 ; PRIOR FILING DATE: 1998-08-04
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 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: 60/098544
 ; PRIOR FILING DATE: 1998-08-31
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 ; PRIOR APPLICATION NUMBER: 60/100038
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 ; PRIOR APPLICATION NUMBER: 60/108787
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 ; PRIOR APPLICATION NUMBER: 60/108801
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 ; PRIOR APPLICATION NUMBER: 60/108849
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; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: 60/113296
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 ; PRIOR APPLICATION NUMBER: 60/134287
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/140650
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/140723
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/141037
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 ; PRIOR APPLICATION NUMBER: 60/144758
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 60/145698
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 ; PRIOR APPLICATION NUMBER: 60/146222
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 ; PRIOR FILING DATE: 1999-11-09
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 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 97.0%; Score 1741.6; DB 15; Length 1837;

Best Local Similarity 99.6%; Pred.No. 0;

Matches 1749; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 32 ACCAGCAGAGCTGGGAGTCTGTAGTTTCTGCTGCGAGGCTCCTGAGGGGAAC 91

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2004, 16:12:03 ; Search time 4851 Seconds
(without alignments)
11055.963 Million cell updates/sec

Title: US-09-997-131-19

Perfect score: 1796

Sequence: 1 ggaaggaggaagtccaagg.....aaaaaaaggcgccgcg 1796

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hrc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hrc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	954.6	53.2	1083	12 BM924147	BM924147 AGENCOURT
2	933.6	52.0	1059	13 BQ073166	BQ073166 AGENCOURT
3	867.8	48.3	988	12 BM922663	BM922663 AGENCOURT
4	837.6	46.6	1075	12 BM923728	BM923728 AGENCOURT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	777.6	43.3	581	12 BI911496	BI911496 603064005
6	715	39.8	737	14 CA307972	CA307972 UI-H-FTI-
7	714.8	39.8	731	14 CD368538	CD368538 UI-H-FTI-
8	692.2	38.5	759	12 BI818421	BI818421 603032889
9	677	37.7	699	12 BM680508	BM680508 UI-E-BJO-
10	620.2	34.5	661	14 CD367917	CD367917 UI-H-FTI-
11	546	30.4	560	9 AW003259	AW003259 wg64f09.x
12	544.8	30.3	568	14 CF541209	CF541209 UI-CF-EC1
13	529.2	29.5	595	12 BI906782	BI906782 603064528
14	521.2	29.0	564	12 CD695911	CD695911 EST12434
15	516	28.7	606	14 CD695740	CD695740 EST12263
16	506	28.2	519	12 BM149897	BM149897 TCAAP3Q10
17	488.2	27.2	490	12 BM147210	BM147210 TCAAP1Q10
18	481.4	26.8	713	12 BI911805	BI911805 603065238
19	469	26.1	469	10 BE673705	BE673705 7d79902.x
20	460.2	25.6	509	12 AW682821	AW682821 UI-E-FTI-
21	459	25.6	460	10 AW236996	AW236996 xm51106.x
22	456.2	25.4	505	12 BM719503	BM719503 UI-E-EJ1-
23	455	25.3	455	10 AW590159	AW590159 hg40c10.x
24	451.2	25.1	458	10 BF478096	BF478096 7d20901.x
25	445.6	24.8	452	10 BE218330	BE218330 hv37c06.x
26	444	24.7	461	9 AI802017	AI802017 tx24d03.x
27	437.4	24.4	451	9 AI707979	AI707979 ag36h01.x
28	421.6	23.5	453	14 CA444183	CA444183 UI-H-DT1-
29	419	23.3	419	10 BF062678	BF062678 7h63910.x
30	418.6	23.3	425	10 AW590572	AW590572 hg46c07.x
31	410.4	22.9	427	9 AI970192	AI970192 wr08d04.x
32	398	22.2	604	12 BI822998	BI822998 603058205
33	393	21.9	860	12 BI768733	BI768733 603058205
34	370.8	20.6	374	10 AW615365	AW615365 hg71d09.x
35	353.4	19.7	363	9 AA984871	AA984871 am62c02.s
36	289.4	16.1	315	9 AI796486	AI796486 wj18f09.x
37	267.6	14.9	1045	11 AK089313	AK089313 Mus muscu
38	252	14.0	690	13 BY747865	BY747865 7h63910.x
39	230.8	12.9	591	13 BQ560405	BQ560405 H4064B05-
40	218	12.1	240	14 CD701327	CD701327 EST17851
41	218	12.1	584	14 CD465049	CD465049 Leukoni1
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43	206.4	11.5	493	10 BF605651	BF605651 272194 MA
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ALIGNMENTS

RESULT 1
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LOCUS- AGENCOURT_6630475 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760369
DEFINITION 5', mRNA sequence.
ACCESSION BM924147 GI:19374526
VERSION BM924147
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1083)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM12807 row: e column: 10
High quality sequence stop: 705.

[illegible]

Db 1033 ATTAGCAGCATTCGCC 1050

RESULT 3
BM922663
LOCUS
DEFINITION
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM922663 988 bp mRNA linear EST 12-MAR-2002
ACENOCURT 6652507 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5755755
5', mRNA sequence.
BM922663 1 GI:19373042
EST.
BM922663 Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 988)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM12795 row: e column: 04
High quality sequence stop: 680.
Location/Qualifiers
1. 988
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5755755"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: pCMV-SPOrt6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."

ORIGIN	Query Match	48.3%	Score 867.8	DB 12	Length 988
	Best Local Similarity	95.7%	Pred. No. 1.4e-140		
	Matches 936	Conservative 6	Mismatches 9	Indels 27	Gaps 4
QY	110	AAGATGCCCTGTGACACTCTACCTGCTCCTCTCTCTGGCTCTCAGGCTACTCCATTGCC	169		
DB	1	AAGATGCCCTGTGACACTCTACCTGCTCCTCTCTCTGGCTCTCAGGCTACTCCATTGCC	60		
QY	170	ACTCAATACCCGGTCCAAACAACAGTGAATGGCTTTGGAGCGGGGCTCTTTGACCGTGCGAG	229		
DB	61	ACTCAATACCCGGTCCAAACAACAGTGAATGGCTTTGGAGCGGGGCTCTTTGACCGTGCGAG	120		
QY	230	TGTTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGGTTCGAGGAGCTATTGG	289		
DB	121	TGTTGTTTACAGATCAGGCTGGGAGACCTACTTGAAGTGGTGGTTCGAGGAGCTATTGG	180		
QY	290	CGTGACTGCAAGATCCCTGTTTAAACCAAGTGGGTACAGCAGGAGGTGAAGAGGGACCGG	349		
DB	181	CGTGACTGCAAGATCCCTGTTTAAACCAAGTGGGTACAGCAGGAGGTGAAGAGGGACCGG	240		
QY	350	GTGTCCATCAGGACAATCAGAAAAACCGCAGCTTCACTGTGACCATGAGGATCTCATG	409		
DB	241	GTGTCCATCAGGACAATCAGAAAAACCGCAGCTTCACTGTGACCATGAGGATCTCATG	300		

QY 1305 TACAATGAACCTTTATTTATTCCTACACATGTTATGGGTGAATATGSCCCCAAG 1364
 Db 666 TACAATGAACCTTTATTTATTCCTACACATGTTATGGGTGAATATGSCCCCAAG 725
 QY 1365 ATATCTGTCTCTTAATCTCTCAGAACTTGTGACTGTTTACCTTCTGTGGCAGAAAGGACAG 1424
 Db 726 ATATCTGTCTCTTAATCTCTCAGAACTTGTGACTGTTTACCTTCTGTGGCAGAAAGGACAG 795
 QY 1425 TGCAGATGATGATTAAGTAAAGACTTTGAGATAGAGAGTTATCTTCTGATGATCAGGTG 1484
 Db 786 TGCAGATGATGATTAAGTAAAGACTTTGAGATAGAGAGTTATCTTCTGATGATCAGGTG 845
 QY 1485 GGGCCAAAATATACCAACAGAGGTCTCTCAT - AAGAAAGAGGCCCAAGAGGTCAAGAGGTA 1543
 Db 845 GGGCCAAAATATACCAACAGAGGTCTCTCAT - AAGAAAGAGGCCCAAGAGGTCCAAAGAGGT 905
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RESULT 5
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 LOCUS 60364005F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213257 5',
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 ACCESSION BI911496
 VERSION BI911496.1 GI:16175248
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 881)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL1535 row: 1 column: 02
 High quality sequence stop: 875.
 Location/Qualifiers
 1..881
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5213257"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_118"
 /note="Vector: PCMV-SF0RT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

FEATURES

source
 Query Match 43.3%; Score 777.6; DB 12; Length 881;
 Best Local Similarity 96.1%; Pred. No. 8.2e-125;
 Matches 844; Conservative 6; Mismatches 20; Indels 8; Gaps 5;
 QY 87 GGAACGGGACCTGTCTGAAGAGAGATGCCCCCTGCTGACACTCTACCTGCTCTCTTCT 146

ORIGIN

Query Match 43.3%; Score 777.6; DB 12; Length 881;
 Best Local Similarity 96.1%; Pred. No. 8.2e-125;
 Matches 844; Conservative 6; Mismatches 20; Indels 8; Gaps 5;

QY 87 GGAACGGGACCTGTCTGAAGAGAGATGCCCCCTGCTGACACTCTACCTGCTCTCTTCT 146

Db 5 GGAACGGGACCTGTCTGAAGAGAGATGCCCCCTGCTGACACTCTACCTGCTCTCTTCT 64
 QY 147 GGCCTCTCAGGCTACTCCATTGCCACTCAAAATCACGGTCCAAACAAACAGTGAATGGCTTGG 206
 Db 65 GGCCTCTCAGGCTACTCCATTGCCACTCAAAATCACGGTCCAAACAAACAGTGAATGGCTTGG 124
 QY 207 AGCGGGCTCTTGAACCGTGCAGTGTGTATACAGATCAGGCTGGGAGACCTACTTGAAGT 266
 Db 125 AGCGGGCTCTTGAACCGTGCAGTGTGTATACAGATCAGGCTGGGAGACCTACTTGAAGT 184
 QY 267 GGTGTGTCTGAGGAGCTATTTGGCGTGTGACTGCAAGATCTTGTAAACACAGTGGGTCAG 326
 Db 185 GGTGTGTCTGAGGAGCTATTTGGCGTGTGACTGCAAGATCTTGTAAACACAGTGGGTCAG 244
 QY 327 AGCAGGAGTGAAGAGGAGCCGGGTGCCATCAAGGCAATCAAGAAACCGCAGCGTTC 386
 Db 245 AGCAGGAGTGAAGAGGAGCCGGGTGCCATCAAGGCAATCAAGAAACCGCAGCGTTC 304
 QY 387 CTGTGACCATGAGGATCTCATGAAACTGATGTGACACTTACTGTGTGGGAATTGAGA 446
 Db 305 CTGTGACCATGAGGATCTCATGAAACTGATGTGACACTTACTGTGTGGGAATTGAGA 364
 QY 447 AAATCTGGAATGACCTTGGGTGCAGTTCAGAGTGCACCTTGCACCAAGCAGTCAACC 506
 Db 365 AAATCTGGAATGACCTTGGGTGCAGTTCAGAGTGCACCTTGCACCAAGCAGTCAACC 424
 QY 507 AAGAAAGAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGCAACAGGCAACAAGC 566
 Db 425 AAGAAAGAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGCAACAGGCAACAAGC 484
 QY 567 TCCTGAAGCTCAGTGTCTCTGCGCCCTCATCTTTCACCATATTKYGVYCTCTTTGGTGG 626
 Db 485 TCCTGAAGCTCAGTGTCTCTGCGCCCTCATCTTTCACCATATTKYGVYCTCTTTGGTGG 544
 QY 627 CGCCTCTACTCTTGGCTTGGAGGATGATGAGTACAGAGAAAGCAGCGGATGTC 686
 Db 545 CGCCTCTACTCTTGGCTTGGAGGATGATGAGTACAGAGAAAGCAGCGGATGTC 604
 QY 687 CAGAG - CAGGTACTGACGCCCTCGAGGGGAGCCTCTGTATGACAGCTGACCCCTG 745
 Db 605 CAGAGNCAGGTACTGACGCCCTCGAGGGGAGCCTCTGTATGACAGCTGACCCCTG 664
 QY 746 CTGSCCGGAACCTCCCGCGA - RAGGCTACCAAGAGCTTTCTCTGCCAGGTGACCA 804
 Db 665 CTGSCCGGAACCTCCCGCGA - RAGGCTACCAAGAGCTTTCTCTGCCAGGTGACCA 724
 QY 805 GGTGAAGTGAATATGTACCATGCTTCTT - GCCGAAGGAGGACA - TTTCCTATG 860
 Db 725 GGTGAAGTGAATATGTACCATGCTTCTT - TGCCGAAGGAGGACAATTTCTTATG 784
 QY 861 CATCTGACCTTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCGCACTCA 920
 Db 785 CATCTGACCTTGGGTGCTGAGGATCAGGAACCGACCTACTGCAACATGGGCGCACTCA 844
 QY 921 GTAGCCAMCTYCCCGGAGGGGCGCTGAGGAGGCCAG 958
 Db 845 GTAGCCAC - TCCCGGAGGGGCGCTGAGGAGGCCCG 880

RESULT 6
 CA307972/c 737 bp mRNA linear EST 01-NOV-2002
 LOCUS UI-H-F71-bib-a-02-0-UI.s1 NCI CGAP.FT1 Homo sapiens cDNA clone
 DEFINITION UI-H-F71-bib-a-02-0-UI 3', mRNA sequence.
 ACCESSION CA307972
 VERSION CA307972.1 GI:24471026
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 737)

AUTHORS
TITLE
JOURNAL
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

FEATURES
 source

Location/Qualifiers
 1..731
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="UI-H-Ftl-bib-a-02-0-UI"
 /tissue_type="Aveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ftl"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP Ftl is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG TISSUE=Human Lung Aveolar Macrophage
 TAG LIB=UI-H-Ftl
 TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 39.8%; Score 715; DB 14; Length 737;
 Best Local Similarity 99.0%; Pred. No. 4.6e-114;
 Matches 729; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1052 CCCCTGCTCCCTCATCAGACCAACCCGGGACTGCTGCTGCTGATCAGCCAGCA 1111
 Db 737 CCCCTGCTCCCTCATCAGACCAACCCGGGACTGCTGCTGCTGATCAGCCAGCA 678
 Qy 1112 TTGCCCTAGCTCTGGGTTGGGCTTGGGCGAAGTCTCAGGGGCTCTAGGAGTTGGG 1171
 Db 677 TTGCCCTAGCTCTGGGTTGGGCTTGGGCGAAGTCTCAGGGGCTCTAGGAGTTGGG 618
 Qy 1172 TTCTTAAACGTCCTCCCTCTCTCATATAGTTGAGGAGGGGCTAGGGATGCTCTGG 1230
 Db 617 TTCTTAAACGTCCTCCCTCTCTCATATAGTTGAGGAGGGGCTAGGGATGCTCTGG 558
 Qy 1231 GGCTTTCATGGGATGATGAAGATGATATGAGAAAAATGTTATCATTTATTCATGAAG 1290
 Db 557 GGCTTTCATGGGATGATGAAGATGATATGAGAAAAATGTTATCATTTATTCATGAAG 498
 Qy 1291 TACATTATCATATACAAAGACCTTTATTTATTCCTACACATGTTATGGCTGAAT 1350
 Db 497 TACATTATCATATACAAAGACCTTTATTTATTCCTACACATGTTATGGCTGAAT 438
 Qy 1351 AATGGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGTGACTGTGTACCTCTGTG 1410

Db 437 AATGGCCCCCAAGATATCTGTCTCTAATCCTCAGAACTTGTGACTGTGTACCTCTGTG 378
 Qy 1411 GCAGAAAGGACAGTGCAGATGTATGTAAGTAAAGACTTTGAGATAGAGAGTTATCT 1470
 Db 377 GCAGAAAGGACAGTGCAGATGTATGTAAGTAAAGACTTTGAGATAGAGAGTTATCT 318
 Qy 1471 TGTGATTCAGTGGGCCCAAAATATCACCACAAGGGTCTCTCATAGAAAGAGCCAGAA 1530
 Db 317 TGTGATTCAGTGGGCCCAAAATATCACCACAAGGGTCTCTCATAGAAAGAGCCAGAA 258
 Qy 1531 GGTCAAGAGGTAGACACAAAGTATGATGGAAGTGGAGCTGGGTGTGACGTGACAGGG 1590
 Db 257 GGTCAAGAGGTAGACACAAAGTATGATGGAAGTGGAGCTGGGTGTGACGTGACAGGG 198
 Qy 1591 GCCATGAATGCCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCTGCTGG 1650
 Db 197 GCATGAATGCCGCGACCTTCAGATGCCAGAAAGGAAAGGAATGGATTCCCTCTGCTGG 138
 Qy 1651 AGCTCCAAAAGAACCCAGCCCTGCCAGCCTTGACCTTGAGCCCATGAAACTGATCTT 1710
 Db 137 AGCTCCAAAAGAACCCAGCCCTGCCAGCCTTGACCTTGAGCCCATGAAACTGATCTT 78
 Qy 1711 GAGCTCTGCGCTCCAGAAATTCAGAGAGATAAAATTTGTTGTTGTTTAAATGAAAAAAA 1770
 Db 77 GAGCTCTGCGCTCCAGAAATTCAGAGAGATAAAATTTGTTGTTGTTTAAATGAAAAAAA 18
 Qy 1771 AAAAAAATAAAAAA 1786
 Db 17 AAAAAAATAAAAAA 2

RESULT 7
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 LOCUS
 UI-H-Ftl-bjw-p-15-0-UI-s1 NCI CGAP Ftl Homo sapiens cDNA clone
 UI-H-Ftl-bjw-p-15-0-UI 3', mRNA sequence.
 CD368538
 CD368538.1 GI:31152628
 EST.
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

JOURNAL
COMMENT

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Prepared by: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 The following repetitive elements were found in this cDNA
 sequence: 24-445, >MLTID#LTR/MaLR (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source

Location/Qualifiers
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 /clone="UI-H-Ftl-bjw-p-15-0-UI"
 /tissue_type="Aveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ftl"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP Ftl is a normalized cDNA library constructed from


```

QY 373 AAACGCGAGTTCACTGTGACCATGAGGATCTCATGAAACTGATGCTGACACTTACTG 432
Db 301 AAACGCGAGTTCACTGTGACCATGAGGATCTCATGAAACTGATGCTGACACTTACTG 360
QY 433 GTGTGGATTGAGAAACTGGAATGACCTGGGCTGACAGTTCAAGTGACACNTGACCC 492
Db 361 GTGTGGATTGAGAAACTGGAATGACCTGGGCTGACAGTTCAAGTGACACNTGACCC 420
QY 493 AGCACAGTCAACCCAGAGAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGGA 552
Db 421 AGCACAGTCAACCCAGAGAACTAGCAGCTCCCAACTCTGACCGGCCACCACTTGGGA 480
QY 553 CAACAGGCAAGCTCTGGAAGCTCAGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Db 481 CAACAGGCAAGCTCTGGAAGCTCAGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 613 GYTGCTTTTGTGGCGGCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
Db 541 GYTGCTTTTGTGGCGGCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 673 AGCCGGAGTGTCCAGAGCAGTACTGCA--GCCCTGGAGGCGGACCTCTGCTATGCA 730
Db 601 AGCCGGAGTGTCCAGAGCAGTACTGCAAGCCCTCGAGGGGCGGACTCTTGTCTATGCA 660
QY 731 GACCTGACCTGCA-GCTGGCGGGAACCTCCCGGAAGCTACCAAGGCTTTCCTC 789
Db 661 GACCTGACCTGCAAGCTGCGGGAACCTCCCGGAAGGCTACCAAGGCTTTCCTC 720
QY 790 TGCCAGGTTGACCAAGTGGAAATATGT 822
Db 721 TGCCAGGTTGACCAAGTGGAAATAT 753

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RESULT 9

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BM680508/c
LOCUS
DEFINITION
  BM680508 699 bp mRNA linear EST 27-FEB-2002
  UI-E-EJ0-aim-f-06-0-UI-s1 UI-E-EJ0 Homo sapiens cDNA clone
  UI-E-EJ0-aim-f-06-0-UI 3', mRNA sequence.
ACCESSION
  BM680508
VERSION
  BM680508.1 GI:18990404
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 699)
  Ronaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
JOURNAL
  9704477
MEDLINE
  8889548
PUBMED
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soaresuiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  The following repetitive elements were found in this cDNA
  sequence: 17-452, >XLRID#LTR/MaLR (matched compliment)
  Seq primer: M13 Forward
  POLYA=yes.
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  Location/Qualifiers
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  /organism="Homo sapiens"
  /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="UI-E-EJ0-aim-f-06-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
  optic nerve, retina, Retina Foveal and Macular, RPE and
  Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/note="Osgan: eye; Vector: pT73-Pac (Pharmacia) with a
  modified polylinker; Site 1: EcoR I; Site 2: Not I;
  UI-E-EJ0 is a subtracted cDNA library constructed
  according to Bonaldo, Lennon and Soares, Genome Research,
  6:791-806, 1996. First strand cDNA synthesis was primed
  with an oligo-dT primer containing a Not I site. Double
  stranded cDNA was ligated to an EcoR I adaptor, digested
  with Not I, and cloned directionally into pT73-Pac
  vector. The oligonucleotide used to prime the synthesis of
  first-strand cDNA contains a library tag sequence that is
  located between the Not I site and the (d)18 tail. The
  sequence tags for this library are: fetal eyes,
  AGAATCAAGA; lens, CGATTAGCA; eye anterior segment,
  AATGGCGAT; optic nerve, CCAATAGTG; retina, CCGCG; Retina
  Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
  library was created for the program, Gene Discovery in the
  Visual System, supported by National Eye Institute (NEI).
  TAG_TISSUE=RPE and Choroid
  TAG_LIB=UI-E-EJ0
  TAG_SEQ=ACCTA"

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ORIGIN

```

Query Match      37.7%; Score 677; DB 12; Length 699;
Best Local Similarity 99.0%; Pred. No. 1.8e-107;
Matches 691; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1090 GCCTCTGCTGATGACCCAGCATTCCTCCCTAGCTCTGGGTTGGGTTGGGCTTC 1149
Db 699 GCCTCTGCTGATGACCCAGCATTCCTCCCTAGCTCTGGGTTGGGTTGGGCTTC 640
QY 1150 AGGGGGCTCTAGGAGTTGGGTTTCTTAAAGTCCCTCTCT-CTACATAGTTGAGA 1208
Db 639 AGGGGGCTCTAGGAGTTGGGTTTCTTAAAGTCCCTCTCTCTCTCATAGTTGAGA 580
QY 1209 GGGGGCTAGGGATATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATAGAAAA 1268
Db 579 GGGGGCTAGGGATATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATAGAAAA 520
QY 1269 TGTTCATATTATTCATGAAGTACCATATCATTAATCAATGAACCTTTATTATGCC 1328
Db 519 TGTTCATATTATTCATGAAGTACCATATCATTAATCAATGAACCTTTATTATGCC 460
QY 1329 TACCACATGTTATGGCTGAATAATGGCCCAAGATATCTGTCTCTTAATCTCAGAA 1388
Db 459 TACCACATGTTATGGCTGAATAATGGCCCAAGATATCTGTCTCTTAATCTCAGAA 400
QY 1389 CTTGTGACTGTTACCTTCTGTGGCAGAAAGGACAGTCAGATGATGATTAAGTAAAGAC 1448
Db 399 CTTGTGACTGTTACCTTCTGTGGCAGAAAGGACAGTCAGATGATGATTAAGTAAAGAC 340
QY 1449 TTTGAGTAGAGAGGTTATTCTTCTGCTGATTTCAGGTGGGCCCAAAATATCACCACAGG 1508
Db 339 TTTGAGTAGAGAGGTTATTCTTCTGCTGATTTCAGGTGGGCCCAAAATATCACCACAGG 280
QY 1509 CTTCTAAGAAGAGGCGCCAGAGGTCAAAGAGGTAGAGACAAAGATGATGATGGAAGTGA 1568
Db 279 CTTCTAAGAAGAGGCGCCAGAGGTCAAAGAGGTAGAGACAAAGATGATGATGGAAGTGA 220
QY 1569 CGTGGGTGTGAGTACGAGGCGGATGAATGCCGAGCCTTCAGATGCCAGAAAGGAA 1628
Db 219 CGTGGGTGTGAGTACGAGGCGGATGAATGCCGAGCCTTCAGATGCCAGAAAGGAA 160
QY 1629 AGGAATGATTCCCTGCTGGAGCCTTCCAAAAGAAACACAGCCCTGCCACGCTTGACT 1688
Db 159 AGGAATGATTCCCTGCTGGAGCCTTCCAAAAGAAACACAGCCCTGCCACGCTTGACT 100

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High quality sequence stop: 477.	High quality sequence stop: 477.
FEATURES	FEATURES
source	source
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/clone="IMAGE:2476073"	/clone="UI-CF-EC1-adz-g-10-0-UI"
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/lab_host="DH10B"	/dev_stage="Adult and Fetal"
/clone_lib="NCI CGAP GC6"	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."	/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGGCTTAC.
ORIGIN	ORIGIN
Query Match	Query Match
Best Local Similarity	Best Local Similarity
Matches 557; Conservative	Matches 557; Conservative
0; Mismatches 0; Indels 1; Gaps 1;	0; Mismatches 0; Mismatches 2; Indels 1; Gaps 1;
QY	QY
1207 GAGGGGCTAGGATATCTCTGGGCTTTCATGGGATGATGAAGATGATGAGAAA	1222 ATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTATT
1266	1281
DB	DB
560 GAGGGGCTAGGATATCTCTGGGCTTTCATGGGATGATGAAGATGATGAGAAA	560 ATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATGAAGAAATGTTATCATTTATT
501	501
QY	QY
1267 AATGTTATCATTTATCATGAAGTACCATTATCATTAATCAATGAACCTTTATTATTG	1282 ATCATGAAGTACCATTTATCATATACATGAACCTTTATTATTGCTTACCATGTTAT
1326	1341
DB	DB
500 AATGTTATCATTTATCATGAAGTACCATTATCATTAATCAATGAACCTTTATTATTG	500 ATCATGAAGTACCATTTATCGTAATACATGAACCTTTATTATTGCTTACCATGTTAT
441	441
QY	QY
1327 CCTACCAATGTTATGGCTGAAATATGGCCCCCAAGATATCTGTGCTCTAATCTTCAG	1342 GGGCTGATAATGGCCCCCAAGATATCTGTGCTCTAATCTCTCAGAACTTGTGACTGTTA
1386	1401
DB	DB
440 CCTACCAATGTTATGGCTGAAATATGGCCCCCAAGATATCTGTGCTCTAATCTTCAG	
381	
QY	QY
1387 AACTGTGACTGTACCTTCTGTGGCAGAAAGGACAGTGCAGATGATGTAAGTTAAGG	
1446	
DB	DB
380 AACTGTGACTGTACCTTCTGTGGCAGAAAGGACAGTGCAGATGATGTAAGTTAAGG	
321	
QY	QY
1447 ACTTGTGATGAGAGGTTATTTCTGTGATTCAGGT-GGGCCCCAAATATCACCAAG	
1505	
DB	DB
320 ACTTGTGATGAGAGGTTATTTCTGTGATTCAGGTGGGGCCCCAAATATCACCAAG	
261	
QY	QY
1506 GGTCTCTATAGAAAGGCGGACAGGTCAAGAGGTAGACAAAGTGTGTAAGT	
1565	
DB	DB
260 GGTCTCTATAGAAAGGCGGACAGGTCAAGAGGTAGACAAAGTGTGTAAGT	
201	
QY	QY
1566 GGAGTGGGTGTGAGTGCAGAGGGGCGCATGAATGCCGCGCCTTCAGATGCCAGAAAGG	
1625	
DB	DB
200 GGAGTGGGTGTGAGTGCAGAGGGGCGCATGAATGCCGCGCCTTCAGATGCCAGAAAGG	
141	
QY	QY
1626 GAAAGGAATGATTCCTGCTGAGGCTCCAAAGAAACCGACCTGCCCGGCTTG	
1685	
DB	DB
140 GAAAGGAATGATTCCTGCTGAGGCTCCAAAGAAACCGACCTGCCCGGCTTG	
81	
QY	QY
1686 ACTTGAGCCCATTTGAAACTGATCTTGAGCTCCTGGCTCCAGAAATTCAGGAGAAAT	
1745	
DB	DB
80 ACTTGAGCCCATTTGAAACTGATCTTGAGCTCCTGGCTCCAGAAATTCAGGAGAAAT	
21	
QY	QY
1746 TTGTGTTGTTTTTAATGA	1763
DB	DB
20 TTGTGTTGTTTTTAATGA	3
RESULT 12	RESULT 12
CF541209/c	CF541209/c
LOCUS	LOCUS
DEFINITION	DEFINITION
UI-CF-EC1-adz-g-10-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone	UI-CF-EC1-adz-g-10-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
ACCESSION	ACCESSION
CF541209	CF541209
VERSION	VERSION
CF541209.1 GI:34593732	CF541209.1 GI:34593732

Db 440 GGGCTGAATATGGCCCCCAAGATATCTGTGTCCTAATCCTCAGAACCTGTGACTGTTA 381
Qy 1402 CTTCTGTGCGAAGAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATGAGA 1461
Db 380 CTTCTGTGCGAAGAGGACAGTGCAGATGATGTAAGTTAAGGACTTTGAGATGAGA 321
Qy 1462 GGTATTATCTTCTGATTCAGTGGGGCCCAAAATATCACCACCAAGGCTCCTCATAGAAAAG 1521
Db 320 GGTATTATCTTCTGATTCAGTGGGGCCCAAAATATCACCACCAAGGCTCCTCATAGAAAAG 261
Qy 1522 AGCCAGAGAGGTCAAGAGGTAGAGCAAAAGTGAATGATGAAAGTGCAGCTGGGTGTGACG 1581
Db 260 AGCCAGAGAGGTCAAGAGGTAGAGCAAAAGTGAATGATGAAAGTGCAGCTGGGTGTGACG 201
Qy 1582 TGACGAGGGCCATGAATCCGAGCCTTCAGATGCCAGAAAGGAAAGGAAATGGATTCC 1641
Db 200 TGACGAGGGCCATGAATCCGAGCCTTCAGATGCCAGAAAGGAAAGGAAATGGATTCC 141
Qy 1642 CTTGCTCTGGAGCCTCCAAAAGAAACACAGCCCTGCCACAGCCTTGACTTGAGCCCATTGAA 1701
Db 140 CTTGCTCTGGAGCCTCCAAAAGAAACACAGCCCTGCCACAGCCTTGACTTGAGCCCATTGAA 81
Qy 1702 ACTGATCTTGAAGCTCTGGGCTCCAGAAATGCAGGAGAAATATGTTGTTGTTTAA 1760
Db 80 ACTGATCTTGAAGCTCTGGGCTCCAGAAATGCAGGAGAAATATGTTGTTGTTTAA 21
Qy 1761 TGAATAAAAAAAAAAAAAA 1780
Db 20 TGAATAAAAAAAAAAAAAA 1

RESULT 13
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LOCUS 603064528F1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5213623 5',
DEFINITION mRNA sequence.
ACCESSION BI906782
VERSION BI906782.1 GI:16169540
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAW1536 row: h column: 08
High quality sequence stop: 595.
Location/Qualifiers
1. 595
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5213623"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

Query Match 29.5%; Score 529.2; DB 12; Length 595;
Best Local Similarity 96.7%; Pred. No. 8.1e-82;
Matches 551; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

ORIGIN

Qy 1217 GGGATATCTCTGGGGCTTCATGGGATGATGAAGATGAATAGAGAAAATGTTATCA 1276
Db 1 GGGATATCTCTGGGGCTTCATGGGAAATGAATGAATGAAGAAAATGTTATCA 59
Qy 1277 TTATTATCATGAAGTACCATTTATCATATACAATGAACCTTTATTTATGCTACCAT 1336
Db 60 TTATTATCATGAAGTACCATTTATCATATACAATGAACCTTTATTTATGCTACCAT 119
Qy 1337 GTTATGGGCTGAATATATGGCCCCCAAGATATCTGTGCTTAATCCTCAGAACCTGTGAC 1396
Db 120 GTTATGGGCTGAATATATGGCCCCCAAGATATCTGTGCTTAATCCTCAGAACCTGTGAC 179
Qy 1397 TGTACCTTCTGTGGCAGAAAGGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGAT 1456
Db 180 TGTACCTTCTGTGGCAGAAAGGGACAGTGCAGATGTATGTAAGTTAAGGACTTTGAGAT 239
Qy 1457 AGAGAGGTTATTTCTGCTGATTCAGGTGGGCCCAAAATATCACCACCAAGGCTCCTATAA 1516
Db 240 AGAGAGGTTATTTCTGCTGATTCAGGTGGGCCCAAAATATCACCACCAAGGCTCCTATAA 299
Qy 1517 GAAAGAGGCCAGAGGTCAAGAGAGGTAGAGCAAAAGTGCATGTAAGTGCAGCTGGGTG 1576
Db 300 GAAAGAGGCCAGAGGTCAAGAGAGGTAGAGCAAAAGTGCATGTAAGTGCAGCTGGGTG 359
Qy 1577 TGACGTGAGCAGGGGCCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGAAATGG 1636
Db 360 TGAAGTGAAGCAGGGGCCCATGAATGCCGAGCTTCAGATGCCAGAAAGGAAAGAAATGG 419
Qy 1637 ATTCCCTGCTGGAGCCCTCCAAAAGAACAGCCCTGCCACAGCTTGAAGTGCAGCTTGA 1696
Db 420 ATTCCCTGCTGGAGCCCTCCAAAAGAACAGCCCTGCCACAGCTTGAAGTGCAGCTTGA 479
Qy 1697 TTGAAGTGAATGATCTTCTGAGCTTCCTGGGCTCCAGAAATTCAGAGGAGAAATAATTTGTTGTTT 1756
Db 480 TTGAAGTGAATGATCTTCTGAGCTTCCTGGGCTCCAGAAATTCAGAGGAGAAATAATTTGTTGTTT 539
Qy 1757 TTGAATGAATAAAAAAAAAAAAAAAAAAAAAA 1786
Db 540 AATGAGCCCAAAAAAAAAAACACAAAAAAAAACA 569

RESULT 14
CD695911
LOCUS CD695911
DEFINITION EST12434 human nasopharynx Homo sapiens cdna, mRNA sequence.
ACCESSION CD695911
VERSION CD695911.1 GI:32221917
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 564)
Zeng, Y.-X., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

Location/Qualifiers

FEATURES

source

1..564

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 29.0%; Score 521.2; DB 14; Length 564;

Best Local Similarity 99.4%; Pred. No. 2e-80; 3; Indels 0; Gaps 0;

Matches 523; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 82 TGAGGGGAACGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACCTGCTCCT 141

Db 39 TGAGGGGAACGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACCTGCTCCT 98

QY 142 CTTCTGGCTCTCAGGCTACTCCATTGCCACTCAAAATCACCGGTCCAAACAGTGAATGG 201

Db 99 CTTCTGGCTCTCAGGCTACTCCATTGTCACTCAAAATCACCGGTCCAAACAGTGAATGG 158

QY 202 CTTGAGGCGGGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTT 261

Db 159 CTTGAGGCGGGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGACCTACTT 218

QY 262 GAAAGTGGTGTGTGAGAGACTATTTGGCGTGAATGCAAGATCCTTTAAACCACTGG 321

Db 219 GAAAGTGGTGTGTGAGAGACTATTTGGCGTGAATGCAAGATCCTTTAAACCACTGG 278

QY 322 GTCAGAGCAGGAGTGAGAGGACCGGTGTCCATCAAGACAAATCAGAAACCGCAC 381

Db 279 GTCAGAGCAGGAGTGAGAGGACCGGTGTCCATCAAGACAAATCAGAAACCGCAC 338

QY 382 GTTCACTGTGACCTGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGAAT 441

Db 339 ATTCACTGTGACCTGAGGATCTCATGAAACTGATGCTGACACTTACTGGTGTGAAT 398

QY 442 TGAGAAACTGGAAATGACCTTGGGTGACAGTTCAAGTAGACCTTGAACCCAGCAGT 501

Db 399 TGAGAAACTGGAAATGACCTTGGGTGACAGTTCAAGTAGACCTTGAACCCAGCAGT 458

QY 502 CACCAAGAAAGAACTAGCAGTCCCAACTCTGACCGGCCACCACTTGACACACAGGCA 561

Db 459 CACCAAGAAAGAACTAGCAGTCCCAACTCTGACCGGCCACCACTTGACACACAGGCA 518

QY 562 CAAGCTCTGAAGCTCAGTGTCTTCCCTGCGCCCTCATCTTCAACATA 607

Db 519 CAAGCTCTGAAGCTCAGTGTCTTCCCTGCGCCCTCATCTTCAACATA 564

RESULT 15

CD695740

LOCUS

CD695740 606 bp mRNA linear EST 25-JUN-2003

DEFINITION

EST12263 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION

CD695740

VERSION

CD695740.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

Transcriptional Gene Expression Profile of Human Nasopharynx

JOURNAL

Unpublished (2003)

COMMENT

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-3770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

FEATURES

source

1..606

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 28.7%; Score 516; DB 14; Length 606;

Best Local Similarity 94.3%; Pred. No. 1.6e-79;

Matches 551; Conservative 2; Mismatches 12; Indels 19; Gaps 1;

QY 15 CAAGGGCGAGATAGTACACAGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAG 74

Db 23 CAAGGGCGAGAGTGTAGTACACAGAGGCTGGGAGTCTGTAGTTTGTCTGCTGCCAG 82

QY 75 GCTCCACTGAGGGGAACGGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACC 134

Db 83 GCTCCACTGAGGGGAACGGGGACCTGTCTGAAGAGAAGATGCCCTGCTGACACTTACC 142

QY 135 TGCTCTCTTCTGGTCTCAGGCTACTCAGTCCACTCAATCACCCTGCTGACACTTACC 194

Db 143 TGCTCTCTTCTGGTCTCAGGCTACTCAGTCCACTCAATCACCCTGCTGACACTTACC 202

QY 195 TGAATGGCTTGGAGCGGGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGA 254

Db 203 TGAATGGCTTGGAGCGGGCTCCTTGACCGTGCAGTGTGTTTACAGATCAGGCTGGGAGA 262

QY 255 CTTACTTGAAGTGGTGTGAGGAGCTATTTGGCGTGAATGCAAGATCCTTGTAAAA 314

Db 263 CTTACTTGAAGTGGTGTGAGGAGCTATTTGGCGTGAATGCAAGATCCTTGTAAAA 322

QY 315 CCAGTGGGTTCAGAGCAGGAGGTGAAGAGGACCGGGTGTGTC-----C 355

Db 323 CCAGTGGGTTCAGAGCAGGAGGTGAAGAGGACCGGGTGTGTC-----C 382

QY 356 ATCAAGGCAATCAGAAAAACCGCACGTTCACTGTGACCATGGAGGATCTCATGAAAACT 415

Db 383 CGAGAGTTCGAGGACACAAACCGCACGTTCACTGTGACCATGGAGGATCTCATGAAAACT 442

QY 416 GATGCTGACACTTACTGGTGTGGAATTCAGAAAACTGGAAATGACCTTGGGGTTCACAGTT 475

Db 443 GATGCTGACACTTACTGGTGTGGAATTCAGAAAACTGGAAATGACCTTGGGGTTCACAGTT 502

QY 476 CAAAGTGACCAATTGACCCAGCAGTCAACCAAGAGAAACTAGCAGTCTCCCAACTCTG 535

Db 503 CAAAGTGACCAATTGACCCAGCAGTCAACCAAGAGAAACTAGCAGTCTCCCAACTCTG 562

QY 536 ACCGCCACCACTTGGACACAGGACCAAGCTCCTGAAGCTCAG 579

Db 563 ACCGCCACCACTTGGACACAGGACCAAGCTCCTGAAGCTCAG 606

Search completed: September 21, 2004, 20:38:45

Job time : 4857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:23:39 ; Search time 121 Seconds
(without alignments)
677.180 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPTLLTYLLFLWLSGVSIAT.....SXLPGRGPPEPEYTSISRP 290
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1493	99.6	290	4 AAB74712	Aab74712 Human mem
2	1493	99.6	290	5 AAU83611	Aau83611 Human PRO
3	1493	99.6	290	6 ABU80758	Abu80758 Human PRO
4	1493	99.6	290	6 ABO33724	Abu33724 Novel hum
5	1493	99.6	290	6 ABU82067	Abu82067 Novel hum
6	1493	99.6	290	6 ABJ72247	Abj72247 Human PRO
7	1493	99.6	290	6 ABJ72375	Abj72375 Human PRO
8	1493	99.6	290	6 ABO34270	Abu34270 Human sec
9	1493	99.6	290	7 ABJ72077	Abj72077 Human mem
10	1493	99.6	290	7 ADB83530	Adb83530 Novel hum
11	1493	99.6	290	7 ADB80636	Adb80636 Novel hum
12	1493	99.6	290	7 ADB73177	Adb73177 Novel hum
13	1493	99.6	290	7 ADB78259	Adb78259 Novel hum
14	1493	99.6	290	7 ADB84907	Adb84907 Human PRO
15	1493	99.6	290	7 ADB78013	Adb78013 Novel hum
16	1493	99.6	290	7 ADB87079	Adb87079 Human PRO
17	1493	99.6	290	7 ADB84661	Adb84661 Human PRO
18	1493	99.6	290	7 ADB83776	Adb83776 Novel hum
19	1493	99.6	290	7 ADB72931	Adb72931 Novel hum
20	1493	99.6	290	7 ADC36769	Adc36769 Human PRO
21	1493	99.6	290	7 ADC21759	Adc21759 Human PRO
22	1493	99.6	290	7 ADC43790	Adc43790 Novel hum
23	1493	99.6	290	7 ADC49898	Adc49898 Novel hum
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26	1493	99.6	290	7 ADC47112	Adc47112 Novel hum
27	1493	99.6	290	7 ADC77987	Adc77987 Novel hum
28	1493	99.6	290	7 ADD05222	Add05222 Novel hum
29	1493	99.6	290	7 ADC77741	Adc77741 Novel hum
30	1493	99.6	290	7 ADD50704	Add50704 Novel hum
31	1493	99.6	290	7 ADD50950	Add50950 Novel hum
32	1493	99.6	290	7 ADD50431	Add50431 Human PRO
33	1493	99.6	290	7 ADD50185	Add50185 Human PRO
34	1493	99.6	290	7 ADD51196	Add51196 Novel hum
35	1493	99.6	290	7 ADC48743	Adc48743 Novel hum
36	1493	99.6	290	8 ADE20914	Ade20914 Novel hum
37	1493	99.6	290	8 ADE05758	Ade05758 Human PRO
38	1493	99.6	290	8 ADD74987	Add74987 Human PRO
39	1493	99.6	290	8 ADD75733	Add75733 Novel hum
40	1493	99.6	290	8 ADD84965	Add84965 Novel hum
41	1493	99.6	290	8 ADD86791	Add86791 Novel hum
42	1493	99.6	290	8 ADE20668	Ade20668 Novel hum
43	1493	99.6	290	8 ADE38965	Ade38965 Novel hum
44	1493	99.6	290	8 ADE05512	Ade05512 Human PRO
45	1493	99.6	290	8 ADD73497	Add73497 Human PRO

ALIGNMENTS

RESULT 1
AAB74712
ID AAB74712 standard; protein; 290 AA.
XX
AC AAB74712;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-18.

XX Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiatherosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX
OS Homo sapiens.

XX WO200112662-A2.

PN 22-FEB-2001.

XX 14-AUG-2000; 2000WO-US022315.

XX 17-AUG-1999; 99US-0149641P.

XX 09-NOV-1999; 99US-0164203P.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

XX Baughm MR, Lu DAM, Patterson C;

XX WPI; 2001-168860/17.

XX N-PSDB; AAF81758.

XX Isolated polypeptide with a human membrane associated protein sequence is useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune/inflammatory, neurological and gastrointestinal disorders.

XX Claim 1; Page 131-132; 173pp; English.

XX AAF81741 to AAF81777 encode the human membrane associated proteins (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic, antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and antiatherosclerotic activities, which can be used in gene therapy. MEMAPs and agonist of MEMAPs can be used to treat a disease or condition associated with decreased expression of functional MEMAP and antagonists

CC of MEMAP are used to treat a disease or condition associated with
 CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated with
 CC MEMAP
 XX
 SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 4; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137; Indels 0; Gaps 0;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTYLLFWLSCYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPLLTYLLFWLSCYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
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 DB 61 DCKILVKTSGSEOEYKRDVSIKONKRTFTVMEDLMKTDADTYMCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTQETSSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 DB 121 VQVTTIDPAPVTQETSSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPQVQLPGLDGLCYADLTQLAGTSRKATTKLSSAQVDQVEYVTMA 240
 DB 181 MKYQQAAGMSPQVQLPGLDGLCYADLTQLAGTSRKATTKLSSAQVDQVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDQETTCNMGLSKLPGRGPPEETETSTISRP 290
 DB 241 SLPKEDISYASLTGAEDQETTCNMGLSKLPGRGPPEETETSTISRP 290
 RESULT 2
 AAU83611
 ID AAU83611 standard; protein; 290 AA.
 XX
 AC AAU83611;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human PRO protein, Seq ID No 40.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 FN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021066.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220585P.
 PR 25-JUL-2000; 2000US-0220605P.
 PR 25-JUL-2000; 2000US-0220607P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.
 PR 25-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-AUG-2000; 2000US-0222425P.
 PR 22-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854280.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI WPI; 2002-172001/22.
 XX N-PSDB; ABK33555.
 DR
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 PS Claim 11; Fig 40; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 5; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTYLLFWLSCYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPLLTYLLFWLSCYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEOEYKRDVSIKONKRTFTVMEDLMKTDADTYMCGIEKTDGNDLGV 120
 DB 61 DCKILVKTSGSEOEYKRDVSIKONKRTFTVMEDLMKTDADTYMCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTQETSSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 DB 121 VQVTTIDPAPVTQETSSSPTLTGHHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPQVQLPGLDGLCYADLTQLAGTSRKATTKLSSAQVDQVEYVTMA 240
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QY 241 SLPKEDISYASLTILGAEDQPTTCNMGXSLXLPGRGPPEPTYSISR 290
DB 241 SLPKEDISYASLTILGAEDQPTTCNMGXSLXLPGRGPPEPTYSISR 290
RESULT 3
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ID ABU80758 standard; protein; 290 AA.
AC AC
XX AC ABU80758;
XX AC
XX 23-JUN-2003 (first entry)
XX Human PRO polypeptide #20.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
KW
XX Homo sapiens.
XX OS
XX US2003036635-A1.
XX 20-FEB-2003.
XX 28-AUG-2002; 2002US-00230163.
XX 25-JUL-2000; 2000US-0220638P.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
XX N-PSDB; ACA66860.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for the manufacture of a medicament for diagnosing or treating
XX tumor.
XX
XX Claim 11; Fig 40; 314pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX useful in diagnostic assays for PRO, by detecting its expression in
XX specific cells, tissues or serum, and for affinity purification of PRO
XX from recombinant cell culture or natural sources. ABU80739-ABU80860
XX represent the human PRO polypeptides of the invention. Note: The sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipdbentry.html
XX
XX Sequence 290 AA;
Query Match 99.6%; Score 1493; DB 6; Length 290;
Best Local Similarity 99.0%; Pred. No. 9,8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCGRGAIWR 60
DB 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERGLTVQCYRSGWETYLKWCGRGAIWR 60
QY 61 DCKILVKTSGSEQVKKRDRVSIKQNKQRTFTVIMEDLMKTDADTYWCGIEKTGNDLGVT 120
DB 61 DCKILVKTSGSEQVKKRDRVSIKQNKQRTFTVIMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLVLLPFIITLILLLVAASLLAWRM 180

DB 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLVLLPFIITLILLLVAASLLAWRM 180
QY 181 MKYQKAAAGMSPEQVLQPLEGDLCLYADLTLOLAGTSRKATTKLSSAQVDQVEYVYVMA 240
DB 181 MKYQKAAAGMSPEQVLQPLEGDLCLYADLTLOLAGTSRKATTKLSSAQVDQVEYVYVMA 240
QY 241 SLPKEDISYASLTILGAEDQPTTCNMGXSLXLPGRGPPEPTYSISR 290
DB 241 SLPKEDISYASLTILGAEDQPTTCNMGXSLXLPGRGPPEPTYSISR 290
RESULT 4
ABO33724
ID ABO33724 standard; protein; 290 AA.
XX AC ABO33724;
XX 17-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO10111.
XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX Homo sapiens.
XX OS
XX US2003045687-A1.
XX 06-MAR-2003.
XX 12-AUG-2002; 2002US-00218631.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-512315/48.
XX N-PSDB; ACD68612.
XX New genes, and its encoded secreted and transmembrane polypeptides,
XX useful for stimulating tumor Necrosis Factor alpha, or chondrocyte, or
XX pericyte proliferation, especially for treating lung tumors, arthritis or
XX wounds in a mammal.
XX
XX Claim 11; Fig 40; 314pp; English.
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
XX 122 PRO (secreted and transmembrane) polypeptides whose sequences are
XX fully defined in the specification; or (b) any of 122 nucleotide
XX sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
XX specification; or the full length coding sequence of any these 122
XX nucleotide sequences. The PRO polypeptides or polynucleotides are useful
XX as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
XX particularly useful for detecting tumours (e.g. lung tumour, colon
XX tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
XX in a mammal, for stimulating the release of TNF-alpha from human blood,
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells, for stimulating proliferation of pericyte cells, or for modulating
XX normal human dermal fibroblast proliferation. The PRO nucleic acid or
XX polypeptide is also useful for treating tumours or various bone and/or
XX cartilage disorders (e.g. sports injuries or arthritis), or wounds. The

CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 XX

SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 6; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTYLLLFWSGYSIATQITGPTTVNGLERGLSVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPLLTYLLLFWSGYSIATQITGPTTVNGLERGLSVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
 QY 121 VQVTTIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 DB 121 VQVTTIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTSTISRP 290
 DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTSTISRP 290

RESULT 5

ABU82067
 ID ABU82067 standard; protein; 290 AA.
 XX
 AC ABU82067;
 XX
 XX
 DT 25-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX
 KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 XX US200308063-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 12-AUG-2002; 2002US-00219003.
 XX
 XX 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-393229/37.
 DR N-PSDB; ACA68516.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 40; 314pp; English.
 XX

XX The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 6; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPLLTYLLLFWSGYSIATQITGPTTVNGLERGLSVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPLLTYLLLFWSGYSIATQITGPTTVNGLERGLSVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
 DB 61 DCKILVKTSGSEQEVKRDVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
 QY 121 VQVTTIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 DB 121 VQVTTIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
 QY 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQKAAAGMSPEQVLPLEGDLQVADLTQAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTSTISRP 290
 DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTSTISRP 290

RESULT 6

ABU72247
 ID ABU72247 standard; protein; 290 AA.
 XX
 AC ABU72247;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 XX Human PRO10111 protein.
 DE
 DE PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
 KW
 XX
 OS Homo sapiens.
 XX
 XX US2003050448-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002US-00230414.
 PF
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR

[illegible][illegible]

KW affinity purification.
 OS Homo sapiens.
 XX US2003044934-A1.
 XX 06-MAR-2003.
 XX 28-AUG-2002; 2002US-00230338.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-492274/46.
 DR N-PSDB; ACD82195.
 XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, or in generating probes.
 XX Claim 19; Fig 40; 315pp; English.
 XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. Nucleic acids that encode PRO can be used to generate either
 CC transgenic animals or knock-out animals useful in developing and
 CC screening of therapeutically useful reagents. The nucleic acids may also
 CC be used in gene therapy for replacing defective gene, in chromosome
 CC identification, as chromosome markers, or in generating probes to isolate
 CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
 CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
 CC and for detecting the presence of tumour in an animal. The PRO
 CC polypeptides are useful as molecular markers for protein electrophoresis
 CC and the isolated nucleic acids may be used for recombinantly expressing
 CC those markers. The PRO polypeptides and nucleic acids may also be used in
 CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
 CC PRO and in affinity purification of PRO from recombinant cell culture or
 CC natural sources. The present sequence represents the amino acid sequence
 CC of a human secreted/transmembrane PRO polypeptide
 XX Sequence 290 AA;
 SQ
 Query Match 99.6%; Score 1493; DB 6; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPELLTYLLFWLSGYSIATQITGTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLTYLLFWLSGYSIATQITGTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQVXRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTDNLGVT 120
 DB 61 DCKILVKTSGSEQVXRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTDNLGVT 120
 QY 121 VQVTDIPAPVQETSSPTLTHLNRHKLKLVLLPLFTIXLLVLAASLLAWRM 180
 DB 121 VQVTDIPAPVQETSSPTLTHLNRHKLKLVLLPLFTIXLLVLAASLLAWRM 180
 QY 181 MKYQKAGMSPQVLPQLEGDLCYADLTQLAGTSRKRATKLSSAQVDQVEVYVTA 240
 DB 181 MKYQKAGMSPQVLPQLEGDLCYADLTQLAGTSRKRATKLSSAQVDQVEVYVTA 240
 QY 241 SLPKEDISYASLTGADQDEPTCNMGLSHLPGRGPPEPTBYSTISRP 290
 DB 241 SLPKEDISYASLTGADQDEPTCNMGLSHLPGRGPPEPTBYSTISRP 290

ABJ72077
 ID ABJ72077 standard; protein; 290 AA.
 XX AC ABJ72077;
 XX 16-OCT-2003 (first entry)
 DT XX
 DE Human membrane bound receptor/protein PRO10111 amino acid sequence.
 XX Human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophin; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX Homo sapiens.
 OS US2003065147-A1.
 XX 03-APR-2003.
 XX 29-AUG-2002; 2002US-00232224.
 XX 28-JUL-1999; 99US-0146222P.
 XX 24-FEB-2000; 2000WO-US005004.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-522018/49.
 DR N-PSDB; AB743901.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for the manufacture of a medicament for diagnosing or treating
 PT tumor.
 XX Claim 11; Fig 40; 315pp; English.
 XX This invention relates to one hundred and twenty two novel nucleic acids
 CC encoding human PRO membrane bound proteins or receptors. Extracellular
 CC proteins play important roles in the formation, differentiation and
 CC maintenance of multicellular organisms. The fate of many individual cells
 CC (for example proliferation, migration or differentiation) is typically
 CC governed by information received from other cells and the immediate
 CC environment. The information is often transmitted by secreted
 CC polypeptides (for example mitogenic factors, survival factors, cytotoxic
 CC factors, differentiation factors, neurotrophins and hormones) which are
 CC received and interpreted by diverse cell receptors or membrane bound
 CC proteins. These membrane bound proteins and receptors may be of use as
 CC pharmaceutical and diagnostic agents, such as in the blocking of receptor
 CC -ligand interactions. The current invention provides the amino acid
 CC sequences of novel human membrane bound receptors and proteins, along
 CC with the cDNA sequences encoding them. The novel proteins of the
 CC invention may have cytostatic activities through the stimulation of
 CC chondrocytes. The nucleic acids of the invention may be useful for the
 CC manufacture of a medicament for diagnosing or treating a tumour in a
 CC mammal. In addition, they may be useful for measuring or detecting the
 CC expression of a tumour associated gene. The present sequence is the amino
 CC acid sequence of a human PRO protein of the invention
 XX Sequence 290 AA;
 SQ
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MPELLTYLLFWLSGYSIATQITGTTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60

Db 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVRSIKDNQKRTFTVTMEDLMKTDADTWGCIETGNDLGV 120
 Db 61 DCKILVKTSGSEQEVKRDVRSIKDNQKRTFTVTMEDLMKTDADTWGCIETGNDLGV 120
 QY 121 VQVTTIDPAPVTOBETSSSPTLTGHHLDNRHKLKLSVLLPLFTIKLLLVVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOBETSSSPTLTGHHLDNRHKLKLSVLLPLFTIKLLLVVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLQPLEGDLQYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTWA 240
 Db 181 MKYQQAAGMSPEQVLQPLEGDLQYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTWA 240
 QY 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTYSISR 290
 Db 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTYSISR 290

RESULT 10

ADB83530

ID ADB83530 standard; protein; 290 AA.

XX ADB83530;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10111.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003073814-A1.

XX 17-APR-2003.

XX 12-AUG-2002; 2002US-00218849.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Deenoyers L, Gerritsen MB, Goddard A, Godowski PU;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;XX WPI; 2003-644806/61.
 DR N-PSDB; ADB83529.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.

XX Claim 11; Fig 40; 315pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1150, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO331, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-

CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1317, PRO1567,
 CC PRO1887, PRO1928, PRO1341, PRO1801, PRO4333, PRO3543, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;

Best Local Similarity 99.0%; Pred. No. 9.8e-137;

Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVRSIKDNQKRTFTVTMEDLMKTDADTWGCIETGNDLGV 120
 Db 61 DCKILVKTSGSEQEVKRDVRSIKDNQKRTFTVTMEDLMKTDADTWGCIETGNDLGV 120
 QY 121 VQVTTIDPAPVTOBETSSSPTLTGHHLDNRHKLKLSVLLPLFTIKLLLVVAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOBETSSSPTLTGHHLDNRHKLKLSVLLPLFTIKLLLVVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLQPLEGDLQYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTWA 240
 Db 181 MKYQQAAGMSPEQVLQPLEGDLQYADLTQLAGTSRKAATTKLSSAQVDQVEVEYVTWA 240
 QY 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTYSISR 290
 Db 241 SLPKEDISYASLTGAEDEPTVCNMGXLSXLPGRGPEEPTYSISR 290

RESULT 11

ADB80636

ID ADB80636 standard; protein; 290 AA.

XX ADB80636;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10111.

XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;

CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVCQYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVCQYRSGWETYLKWCRCGAIWR 60
 Qy 61 DCKILVKTSGSEFQVKDRVSIKQNKRTFTVMTEDLTKMDADTYWCGTEKTNLDLGV 120
 Db 61 DCKILVKTSGSEFQVKDRVSIKQNKRTFTVMTEDLTKMDADTYWCGTEKTNLDLGV 120
 Qy 121 VQVITDPAPVQTEETSSPTTGHLDNRHKLKLSVLLPLFIPTILLVAASLLAWRM 180
 Db 121 VQVITDPAPVQTEETSSPTTGHLDNRHKLKLSVLLPLFIPTILLVAASLLAWRM 180
 Qy 181 MKYQKAGMSPFQVLPLEGDLVADLTQLAGTSRKATTKLSSAQDVQVEVEYVTMA 240
 Db 181 MKYQKAGMSPFQVLPLEGDLVADLTQLAGTSRKATTKLSSAQDVQVEVEYVTMA 240
 Qy 241 SLPKEDISYASLTGAEDEPTTCNMGLSKSLPGRGPPEETESTTSR 290
 Db 241 SLPKEDISYASLTGAEDEPTTCNMGLSKSLPGRGPPEETESTTSR 290
 RESULT 13
 ADB78259
 ID ADB78259 standard; protein; 290 AA.
 XX
 AC ADB78259;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10111.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;

KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003092889-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 13-AUG-2002; 2002US-00219478.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021056.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Deenover L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-765495/72.
 DR N-PSDB; ADB78258.
 XX
 DR New isolated PRO polypeptide useful for tissue typing, gene therapy, as
 PT molecular weight markers in protein electrophoresis, and for treating
 PT arthritis and tumors.
 PT
 PS Claim 11; Fig 40; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 290 AA;
 Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVCQYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVCQYRSGWETYLKWCRCGAIWR 60

CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identifications, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.

XX
SQ Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;
Best Local Similarity 99.0%; Pred. No. 9.8e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITPTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITPTVNGLSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTDIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTDIDPAPVTOETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLLVAASLLAWRM 180

QY 181 MXYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSPRKATKLSSAQVDQVEYVTMA 240
Db 181 MXYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSPRKATKLSSAQVDQVEYVTMA 240

QY 241 SLPKEDISYASLTGAEDQPTCYNMGXLSXLPGRGPEETEXTISRP 290
Db 241 SLPKEDISYASLTGAEDQPTCYNMGXLSXLPGRGPEETEXTISRP 290

RESULT 14
ADB84907
ID ADB84907 standard; protein; 290 AA.
AC ADB84907;
DT 04-DEC-2003 (first entry)
DE Human PRO polypeptide #20.
KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
KW cancer; lung; colon; breast; prostate; rectum; liver;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW arthritis; sports injury; cytostatic; antiarthritic.
OS Homo sapiens.
PN US2003073817-A1.
PD 17-APR-2003.
PF 26-AUG-2002; 2002US-00227883.
PR 01-AUG-2000; 2000US-0222425P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-APR-2002; 2002US-00119480.
PA (GETH) GENENTECH INC.
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
DR WPI; 2003-730024/69.
DR N-PSDB; ADB84906.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful e.g. in gene therapy, disease diagnosis, chromosome identification and tissue typing.
PS Claim 11; Fig 40; 314pp; English.
XX The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating

RESULT 15
ADB78013
ID ADB78013 standard; protein; 290 AA.
AC ADB78013;
XX 04-DEC-2003 (first entry)
DT
DE Novel human secreted and transmembrane protein PRO10111.
KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
KW antiarthritic; pericyte cell proliferation;
KW chondrocyte cell differentiation; chondrocyte cell proliferation;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX US2003092886-A1.
PN
XX 15-MAY-2003.
PD
XX 09-AUG-2002; 2002US-00216165.
PF
XX 25-JUL-2000; 2000US-0220607P.
PR
XX 01-JUN-2001; 2001WO-US017800.
PR
XX 29-JUN-2001; 2001WO-US021066.
PR
XX 09-APR-2002; 2002US-00119480.
XX

PA (GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 FI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-765494/72.
 DR N-PSDB; ADB78012.
 XX

PT Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as
 FT molecular weight markers in protein electrophoresis, for treating
 FT arthritis, tumor.
 XX

PS Claim 11; Fig 40; 308pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO1229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO331, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1486, PRO4302, PRO4408,
 CC PRO5723, PRO5725, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 290 AA;

Query Match 99.6%; Score 1493; DB 7; Length 290;
 Best Local Similarity 99.0%; Pred. No. 9.8e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPILTLVLLFWLSGYSTATQITGPTVNGLSLTQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MELLTLVLLFWLSGYSTATQITGPTVNGLSLTQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVWMDLMKTDADTYWCGIEKTGNDLGVT 120
 QY 121 VQVITDPAPVTQETSSPFTTGHHLNRRHKLKLSVLLPLIFTIXILLVVAASLLAWRM 180
 Db 121 VQVITDPAPVTQETSSPFTTGHHLNRRHKLKLSVLLPLIFTIXILLVVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVQLPGLDLCVADLTQLAGTSPRKATTKLSSAQVQVEVEYVTMA 240
 Db 181 MKYQQAAGMSPEQVQLPGLDLCVADLTQLAGTSPRKATTKLSSAQVQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290

Search completed: September 16, 2004, 12:37:17
 Job time : 125 secs

Db 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:39:56 ; Search time 131 Seconds
(without alignments)
710.906 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 1499
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 32113274 residues

Total number of hits satisfying chosen parameters: 1342398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1493	99.6	290	9	US-09-965-529-18
2	1493	99.6	290	10	US-09-969-680A-18
3	1493	99.6	290	12	US-10-219-535-40
4	1493	99.6	290	12	US-10-232-230-40
5	1493	99.6	290	12	US-10-232-224-40
6	1493	99.6	290	14	US-10-237-884-40
7	1493	99.6	290	14	US-10-230-163-40
8	1493	99.6	290	14	US-10-230-338-40
9	1493	99.6	290	14	US-10-218-631-40
10	1493	99.6	290	14	US-10-230-414-40
11	1493	99.6	290	14	US-10-216-159A-40
12	1493	99.6	290	14	US-10-218-849-40
13	1493	99.6	290	14	US-10-227-873-40
14	1493	99.6	290	14	US-10-227-883-40
15	1493	99.6	290	14	US-10-219-076-40

16	1493	99.6	290	14	US-10-230-434-40
17	1493	99.6	290	14	US-10-219-003-40
18	1493	99.6	290	14	US-10-219-075-40
19	1493	99.6	290	14	US-10-219-484-40
20	1493	99.6	290	14	US-10-219-466-40
21	1493	99.6	290	14	US-10-219-479-40
22	1493	99.6	290	14	US-10-219-481-40
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29	1493	99.6	290	14	US-10-219-478-40
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31	1493	99.6	290	14	US-10-233-205-40
32	1493	99.6	290	14	US-10-219-072-40
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35	1493	99.6	290	14	US-10-219-524-40
36	1493	99.6	290	14	US-10-219-528-40
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44	1493	99.6	290	14	US-10-232-229-40
45	1493	99.6	290	14	US-10-232-234-40

ALIGNMENTS

RESULT 1
US-09-965-529-18
; Sequence 18, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1562471CD1
US-09-965-529-18

Query Match 99.6%; Score 1493; DB 9; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSGISITVOCVYRSQWETVLYKWCRAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSGISITVOCVYRSQWETVLYKWCRAIWR 60

QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
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 QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290
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RESULT 2

US-09-969-680A-18
 ; Sequence 18, Application US/09969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yaida
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969,680A
 ; CURRENT FILING DATE: 2003-10-02
 ; PRIOR APPLICATION NUMBER: US00/22315
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149,641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164,203
 ; PRIOR FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 1562471CD1
 US-09-969-680A-18

Query Match 99.6%; Score 1493; DB 10; Length 290;
 Best Local Similarity 99.0%; Pred. No. 2.9e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
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RESULT 3
 US-10-219-535-40
 ; Sequence 40, Application US/10219535
 ; Publication No. US20040044179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Garney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC60
 ; CURRENT APPLICATION NUMBER: US/10/219,535
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 40
 ; LENGTH: 290
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-219-535-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
 Best Local Similarity 99.0%; Pred. No. 2.9e-137;
 Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTYLLLFWSLGSYIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTYLLLFWSLGSYIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 Db 61 DCKILVKTSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGV 120
 QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLCTYADLTQLAGTSPRKATTKLSSAQVDQVEEYVTMA 240
 Db 181 MKYQQAAGMSPEQVLPQLEGDLCTYADLTQLAGTSPRKATTKLSSAQVDQVEEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290
 Db 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTYSTISRP 290

Db 241 SLPKEDI SYASLTGAEDEPTCYCNMGHLSHLFGRGPEEPTYSTISRP 290

RESULT 4

US-10-232-230-40
; Sequence 40, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C103
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTYLLFWLSGYSIATQITGPTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVKKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQVKKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOEFTSSPTLGHLDNRHLLKLSVLLPLIFTXILLVAASLLAWRM 180
DB 121 VQVTTIDPAPVTOEFTSSPTLGHLDNRHLLKLSVLLPLIFTXILLVAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPEKATTKLSSAQDQVEVEYVTMA 240
DB 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPEKATTKLSSAQDQVEVEYVTMA 240
QY 241 SLPKEDI SYASLTGAEDEPTCYCNMGHLSHLFGRGPEEPTYSTISRP 290

RESULT 5

US-10-232-224-40
; Sequence 40, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-40

Query Match 99.6%; Score 1493; DB 12; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTYLLFWLSGYSIATQITGPTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVKKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQVKKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOEFTSSPTLGHLDNRHLLKLSVLLPLIFTXILLVAASLLAWRM 180
DB 121 VQVTTIDPAPVTOEFTSSPTLGHLDNRHLLKLSVLLPLIFTXILLVAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPEKATTKLSSAQDQVEVEYVTMA 240
DB 181 MKYQQAAGMSPQVLPLEGDLQVADLTQLAGTSPEKATTKLSSAQDQVEVEYVTMA 240
QY 241 SLPKEDI SYASLTGAEDEPTCYCNMGHLSHLFGRGPEEPTYSTISRP 290

Db 241 SLPKEDISASLTGADEPTCYCNHGLSHLPGRGPETEXTSTSRP 290
RESULT 6
US-10-227-884-40
; Sequence 40, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

QY 121 VQVTDPAVTOBETSSPTLTGHLNDRHKLKSVLLPLFTIXLILLVVAASLLAWRM 180
Db 121 VQVTDPAVTOBETSSPTLTGHLNDRHKLKSVLLPLFTIXLILLVVAASLLAWRM 180
QY 181 MKYQKAGMSPEQVLPGLGDLGVADTLQAGTSRKAATKLSAQDOVEVEYVTMA 240
Db 181 MKYQKAGMSPEQVLPGLGDLGVADTLQAGTSRKAATKLSAQDOVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTYCNMGXLSXLPGRQPEEPTTYSTISRP 290
Db 241 SLPKEDISYASLTGAEDEPTYCNMGXLSXLPGRQPEEPTTYSTISRP 290

RESULT 7
US-10-230-163-40
; Sequence 40, Application US/10230163
; Publication No. US2003036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905

QY 121 VQVTDPAVTOBETSSPTLTGHLNDRHKLKSVLLPLFTIXLILLVVAASLLAWRM 180
Db 121 VQVTDPAVTOBETSSPTLTGHLNDRHKLKSVLLPLFTIXLILLVVAASLLAWRM 180
QY 181 MKYQKAGMSPEQVLPGLGDLGVADTLQAGTSRKAATKLSAQDOVEVEYVTMA 240
Db 181 MKYQKAGMSPEQVLPGLGDLGVADTLQAGTSRKAATKLSAQDOVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTYCNMGXLSXLPGRQPEEPTTYSTISRP 290
Db 241 SLPKEDISYASLTGAEDEPTYCNMGXLSXLPGRQPEEPTTYSTISRP 290

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGEQEVRDRVSIKQKQKRTFTVWMDLMKTDADTYWCGIEKTDNDLGV 120
Db 61 DCKILVKTSGEQEVRDRVSIKQKQKRTFTVWMDLMKTDADTYWCGIEKTDNDLGV 120

PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/098596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. NO. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNOKNRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNOKNRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
QY 121 VQVTTDPAPVTOEETSSPTLTGHHLNDRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
Db 121 VQVTTDPAPVTOEETSSPTLTGHHLNDRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
QY 181 MKYQKAAAGSPQVLOPLEGDIQYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKAAAGSPQVLOPLEGDIQYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDQPTTCNMGXLSXLPGRGPPEPTETYSISR 290
Db 241 SLPKEDISYASLTGAEDQPTTCNMGXLSXLPGRGPPEPTETYSISR 290

RESULT 8
US-10-230-338-40
; Sequence 40, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-40

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;

Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNOKNRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNOKNRTFTVTMEDLMKTDADTYKCGIEKTGNDLGV 120
QY 121 VQVTTDPAPVTOEETSSPTLTGHHLNDRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
Db 121 VQVTTDPAPVTOEETSSPTLTGHHLNDRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
QY 181 MKYQKAAAGSPQVLOPLEGDIQYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKAAAGSPQVLOPLEGDIQYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDQPTTCNMGXLSXLPGRGPPEPTETYSISR 290
Db 241 SLPKEDISYASLTGAEDQPTTCNMGXLSXLPGRGPPEPTETYSISR 290

RESULT 9
US-10-218-631-40
; Sequence 40, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-40

Query Match 99.6%; Score 1493; DB 14; Length 290;

Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSQEVEKRDVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSQEVEKRDVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTTIDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
DB 121 VQVTTIDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180

QY 181 MKYQKKAAGMSPEQVLQLEGDLGYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQKKAAGMSPEQVLQLEGDLGYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290
DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290

RESULT 10

US-10-230-414-40
; Sequence 40, Application US/10230414
; Publication No. US2003005048A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-40

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSQEVEKRDVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSQEVEKRDVSIKQKQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTTIDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
DB 121 VQVTTIDPAPVTQETSSPTLTGHHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180

QY 181 MKYQKKAAGMSPEQVLQLEGDLGYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQKKAAGMSPEQVLQLEGDLGYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290
DB 241 SLPKEDISYASLTGAEQDEPTYCNMGXLSXLPGRGPEEPTYSTISRP 290

RESULT 11

US-10-216-159A-40
; Sequence 40, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-40

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTNDLGVT 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTNDLGVT 120
QY 121 VQVITDPAPVTOETSSPTLGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
DB 121 VQVITDPAPVTOETSSPTLGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGSPQVQLPQLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQQAAGSPQVQLPQLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGABDQFTYCNMGHLSLHPGRGPPEPTYSTISRP 290
DB 241 SLPKEDISYASLTGABDQFTYCNMGHLSLHPGRGPPEPTYSTISRP 290

RESULT 12
US-10-218-849-40
; Sequence 40, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691

Query Match 99.6%; Score 1493; DB 14; Length 290;
Best Local Similarity 99.0%; Pred. No. 2.9e-137;
Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTNDLGVT 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTNDLGVT 120
QY 121 VQVITDPAPVTOETSSPTLGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
DB 121 VQVITDPAPVTOETSSPTLGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQQAAGSPQVQLPQLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQQAAGSPQVQLPQLEGDLQYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 99.6%; Score 1493; DB 14; Length 290;

Best Local Similarity 99.0%; Pred.No.2.9e-137;

Matches 287; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLRSGLTVQCVYSGWETYLKWCRCGAIWR 60

Db 1 MPLLTLVLLFWLSGYSIATQITGTTVNGLRSGLTVQCVYSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEBVKRDRVSIKQNKRTFTVTMEDLMKTDADTYWCGIEKTDGLGVT 120

Db 61 DCKILVKTSGSEVQRDRVSFKDQKXRTFTVTWEDLMKTDADTYWCGIEKGTNDLGV 120
QY 121 VQVTTIDPAPVTOBESSSTLTGCHLDNRHKLLKLSVLLPLFTIXLLVLAASLLAWRM 180
Db 121 VQVTTIDPAPVTOBESSSTLTGCHLDNRHKLLKLSVLLPLFTIXLLVLAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLQPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLQPLEGDLVADLTLOAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISVASLTGAEDEPTCYCNGXLSXLPGRGPPEPTXSTISRP 290
Db 241 SLPKEDISVASLTGAEDEPTCYCNGXLSXLPGRGPPEPTXSTISRP 290

RESULT 14

US-10-227-893-40
; Sequence 40, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F530P1C78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787

Query Match		99.6%;	Score 1493;	DB 14;	Length 290;
Best Local Similarity		99.0%;	Pred. No. 2.9e-137;		
Matches 287;	Conservative	0;	Mismatches 3;	Indels	0; Gaps 0;
QY	1	MPLLTLVLLFWLSGYSIATQITGPTTVNGLRGSITVQCVYRSGWETYLKWCRCGAIWR	60		
Db	1	MPLLTLVLLFWLSGYSIATQITGPTTVNGLRGSITVQCVYRSGWETYLKWCRCGAIWR	60		
QY	61	DKILVKTSGSEQEVKRDVRSIKDNOKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT	120		
Db	61	DKILVKTSGSEQEVKRDVRSIKDNOKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT	120		
QY	121	VQVTIDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIPTIXILLVVAASLIAMRM	180		
Db	121	VQVTIDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIPTIXILLVVAASLIAMRM	180		
QY	181	MKYQQAAGNSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVINA	240		
Db	181	MKYQQAAGNSPEQVLQPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVINA	240		
QY	241	SLPKEDISYASLTIGAEDQDEPTYCMMGXISSXLPGRGPPEPTTEYSTISRP	290		
Db	241	SLPKEDISYASLTIGAEDQDEPTYCMMGXISSXLPGRGPPEPTTEYSTISRP	290		

Search completed: September 16, 2004, 12:51:46
Job time : 133 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:32:35 ; Search time 41 Seconds
(without alignments)
680.379 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPLLTLVLLFWLSGYSIAT.....SXLPGRGPPEPTSTISRP 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 781.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	231	15.4	228	2	JC7761	dendritic cell-der
2	224.5	15.0	224	2	I37243	CMRP-35 antigen -
3	159.5	10.6	773	1	QRREG	secretory componen
4	145.5	9.7	769	1	QRRTGS	secretory componen
5	134.5	9.0	764	1	QRHUGS	secretory componen
6	132.5	8.8	757	1	S48841	polymERIC immunogl
7	131.5	8.8	757	2	I45956	T-cell receptor de
8	129.5	8.6	292	2	S03421	T-cell receptor de
9	128.5	8.6	142	2	S04634	T-cell receptor de
10	127.5	8.5	293	2	R40131	T-cell receptor de
11	127	8.5	157	2	S04915	rearranged T-cell
12	126.5	8.4	138	2	I46634	rearranged T-cell
13	126	8.4	137	2	I46628	rearranged T-cell
14	125	8.3	145	2	I46633	T-cell receptor de
15	124.5	8.3	131	2	S36301	T-cell receptor de
16	119.5	8.0	115	2	B32071	T-cell receptor de
17	116.5	7.8	135	2	S36288	T-cell receptor de
18	115.5	7.7	142	2	S36316	T-cell receptor de
19	115.5	7.7	145	2	S36299	T-cell receptor de
20	115.5	7.7	149	2	S36317	T-cell receptor de
21	114.5	7.6	146	2	S36323	T-cell receptor de
22	110.5	7.4	143	2	S36300	T-cell receptor de
23	108.5	7.2	132	2	I46640	rearranged T-cell
24	108.5	7.2	136	2	I46635	rearranged T-cell
25	108.5	7.2	137	2	S36311	T-cell receptor de
26	107.5	7.2	143	2	S36321	T-cell receptor de
27	106.5	7.1	142	2	S36310	T-cell receptor de
28	106.5	7.1	142	2	S36309	T-cell receptor de
29	105	7.0	151	2	I46626	rearranged T-cell

30 105 7.0 271 2 A53268 T-cell receptor al
31 105 7.0 451 2 S71754 cellular hepatitis
32 104.5 7.0 142 2 S36307 T-cell receptor de
33 104.5 7.0 145 2 I46629 rearranged T-cell
34 104.5 7.0 145 2 I46639 rearranged T-cell
35 102 6.8 128 2 S46372 IG light chain var
36 101 6.7 139 2 I46630 rearranged T-cell
37 99.5 6.6 133 2 I46632 rearranged T-cell
38 99 6.6 129 1 KIHUWK IG kappa chain pre
39 99 6.6 143 2 JI0082 T-cell receptor de
40 99 6.6 841 2 JC5894 killer cell inhibi
41 98.5 6.6 120 2 S36306 T-cell receptor de
42 98.5 6.6 135 2 S57892 T-cell receptor de
43 98.5 6.6 144 2 S36308 T-cell receptor de
44 98.5 6.6 145 2 I46631 rearranged T-cell
45 98.5 6.6 1694 2 S50065 sialoadhesin - mou

ALIGNMENTS

RESULT 1

JC7761
dendritic cell-derived immunoglobulin(Ig)-like receptor 1.DIGR1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7761
R: Luo, K.; Zhang, W.; Sui, L.; Li, N.; Zhang, M.; Ma, X.; Zhang, L.; Cao, X.
Biochem. Biophys. Res. Commun. 287, 35-41, 2001
A:Title: DIGR1, a novel membrane receptor of the immunoglobulin gene superfamily, is pre
A:Reference number: JC7761; PMID:11549249
A:Contents: Dendritic cells
A:Accession: JC7761
A:Molecule type: mRNA
A:Residues: 1-228 <LUO>
A:Cross-references: GB:AY048685
C:Comment: This protein, a cell surface type I transmembrane glycoprotein of membrane re
functions in the immunobiology of antigen-presenting cells.
C:Genetics:
A:Gene: digr1
C:Keywords: glycoprotein

Query Match 15.4%; Score 231; DB 2; Length 228;
Best Local Similarity 36.7%; Pred. No. 6.6e-12;
Matches 58; Conservative 26; Mismatches 52; Indels 22; Gaps 6;

QY 8 LLLFWLSGYSIATQIT-----GPTTVANGLERGSLTVOCVYRSGWETYLKWRCGAIWRD 61
Db 5 VRLWLPNALFLSQVPGCVPLHGPSTITGAVGESLSVSCQYEEKFKTKDKFWCGLKVL 64
QY 62 CKILVKTSGSEQEVKRDVRSIKDNOKNRTFTVTMEDLMKKTADTWTCCGIE-----KTGN 115
Db 65 CKDIVKTSSE-EVANGRTVIRDPDNLFTFTVYESLTLEDADTYMCAVDISLGDGSLGF 123
QY 116 DLGVTQVITDPA--PVTQETSS-----SPTLT-GH 144
Db 124 DKYFKIEUSVPSDPVTGSSLESGRDILESPTSSVGH 161

RESULT 2

I37243
CMRP-35 antigen - human
C:Species: Homo sapiens (nan)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I37243
R: Jackson, D.G.; Hart, D.N.; Starling, G.; Bell, J.I.
Eur. J. Immunol. 22, 1157-1163, 1992
A:Title: Molecular cloning of a novel member of the immunoglobulin gene superfamily homo
A:Reference number: I37243; PMID:92249405; PMID:1349532
A:Accession: I37243
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-224 <RES>

Db 180 TEYVDPYKDKRAILFMKGTSRDIPYVNIISHLIPSDAGLYVCQ-----AGSGPSADKN 231

Qy 194 ----QVLOPEGGDLCYADLTQLQA-----GTSRKAATKLSSAQVDQVEVYVTMAS--- 241

Db 232 NADLQVLEP-EPELLYKDLRSSVTFECDLGREVANDAKYLCRNKKTCDVIINTLGRKDP 290

Qy 242 -----LPKEDIS-YASLTGAEDEQEPYCNMGXSSXLPGRG 277

Db 291 APEGRIILTPDDNGRFSVLTGLRKEDAGHYQCGAIISSGLPQEG 335

RESULT 5

ORHUGS

A;Title: secretory component precursor [validated] - human

N;Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

K;Contains: free secretory component; transmembrane secretory component

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence revision 23-Aug-1996 #text change 08-Dec-2000

C;Accession: A46537; A55284; I38115; A32263; S38978; S13453; A02112

R;Krajci, P.; Kvale, D.; Tasken, K.; Brandtzaeg, P.

Eur. J. Immunol. 22, 2309-2315, 1992

A;Title: Molecular cloning and exon-intron mapping of the gene encoding human transmembrane secretory component

A;Reference number: A46537; MUID:92387236; PMID:1335431

A;Accession: A46537

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-764 <KRA>

A;Cross-references: GB:843449; NID:G255097; PIDN:AA23176.1; PID:G255098

A;Experimental source: leukocytes

A;Note: sequence extracted from NCBI backbone (NCBIP:113253)

R;Krajci, P.; Grzeschik, K.H.; Geurts van Kessel, A.H.; Olaisen, B.; Brandtzaeg, P. Hum. Genet. 87, 642-648, 1991

A;Title: The human transmembrane secretory component (poly-Ig receptor): molecular cloning and exon-intron mapping

A;Reference number: A55284; MUID:92039621; PMID:1682231

A;Accession: A55284

A;Molecule type: mRNA

A;Residues: 1-764 <KR2>

A;Cross-references: GB:862403; NID:G238235; PIDN:AA20203.1; PID:G238236

A;Experimental source: colonic adenocarcinoma cell line

A;Note: sequence extracted from NCBI backbone (NCBIN:62403, NCBIP:62408)

R;Piskurich, J.F.; France, J.A.; Tamer, C.M.; Willmer, C.A.; Kaetzel, C.S.; Kaetzel, D.M. Mol. Immunol. 30, 413-421, 1993

A;Title: Interferon-gamma induces polymeric immunoglobulin receptor mRNA in human intest

A;Reference number: I38115; MUID:93205018; PMID:8455639

A;Accession: I38115

A;Molecule type: mRNA

A;Residues: 1-764 <RES>

A;Cross-references: EMBL:X73079; NID:G456345; PIDN:CAA51532.1; PID:G456346

A;Note: submitted to the EMBL/Genbank/DBJ databases by J.F. Piskurich, February 1994

R;Krajci, P.; Solberg, R.; Sandberg, M.; Oyen, O.; Jahnson, T.; Brandtzaeg, P. Biochem. Biophys. Res. Commun. 158, 783-789, 1989

A;Title: Molecular cloning of the human transmembrane secretory component (poly-Ig recep

A;Reference number: A32263; MUID:89149795; PMID:2920039

A;Accession: A32263

A;Molecule type: mRNA

A;Residues: 72-764 <KR3>

A;Cross-references: GB:M24559; NID:G514365; PIDN:AAA36102.1; PID:G514366

R;Fallgreen-Gebauer, E.; Gebauer, W.; Bastian, A.; Kratzin, H.D.; Biffert, H.; Zimmermann, H. Biol. Chem. Hoppe-Seyler 374, 1023-1028, 1993

A;Title: The covalent linkage of secretory component to IgA. Structure of sIgA.

A;Reference number: S38978; MUID:94121784; PMID:8292260

A;Accession: S38978

A;Molecule type: protein

A;Residues: 478-488; 517-526; 543-545 <FAL>

A;Note: disulfide bonds for unbound and IgA-bound forms

R;Eiffert, H.; Quentn, E.; Wiederhold, M.; Hillemeir, S.; Decker, J.; Weber, M.; Hilsch Biol. Chem. Hoppe-Seyler 372, 119-128, 1991

A;Title: Determination of the molecular structure of the human free secretory component.

A;Reference number: S13453; MUID:91315750; PMID:1859628

A;Accession: S13453

A;Molecule type: protein

A;Residues: 19-135; 'Q', 137-157; 'D', 159-207; 'DE', 210-228; 230-233; 'N', 235-240; 'Q', 242-261; R;Eiffert, H.; Quentn, E.; Decker, J.; Hillemeir, S.; Hufschmidt, M.; Klingmuller, D.;

Hoppe-Seyler's Z. Physiol. Chem. 365, 1489-1495, 1984

A;Title: The primary structure of the human free secretory component and the arrangement

A;Reference number: A02112; MUID:85128981; PMID:8526384

A;Accession: A02112

A;Molecule type: protein

A;Residues: 19-157; 'D', 159-207; 'DE', 210-228; 230-233; 'N', 235-240; 'Q', 242-261; 'Q', 263-279; A;Note: paper in German with English abstract

C;Comment: As a 100K transmembrane receptor for polymeric immunoglobulins, secretory com

ylated, forms interchain disulfide bonds, undergoes proteolysis and transcytosis. Free s

C;Genetics:

A;Gene: GDB:PIGR

A;Cross-references: GDB:120290; OMIM:173880

A;Map position: 1q31-q41

A;Introns: 15/1; 130/1; 349/1; 460/1; 569/1; 629/2; 670/1; 714/1; 733/3

A;Note: the first intron occurs before the initiator codon

C;Complex: monomeric as a transmembrane receptor or free in mucosal secretions; heterode

amers; hetero-22-mer composed of one chain of secretory component, one chain of immunogl

C;Superfamily: secretory component; immunoglobulin homology

C;Keywords: duplication; glycoprotein; immunoglobulin receptor; phosphoprotein; transcyt

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-764/Product: transmembrane secretory component #status predicted <WATM>

F;19-577/Product: free secretory component #status experimental <WAT>

F;33-112/Domain: immunoglobulin homology <IM1>

F;145-222/Domain: immunoglobulin homology <IM2>

F;250-327/Domain: immunoglobulin homology <IM3>

F;364-443/Domain: immunoglobulin homology <IM4>

F;475-546/Domain: immunoglobulin homology <IM5>

F;639-661/Domain: transmembrane #status predicted <TMM>

F;662-764/Domain: intracellular #status predicted <INT>

F;40-110;56-64;152-220;257-325;271-279;371-441;385-395;482-544;496-503/Disulfide bonds:

F;83;90;135;186;421;469;499/Binding site: carbohydrate (Asn) (covalent) #status experime

F;486-520/Disulfide bonds: (in Ig-unbound form) #status experimental

F;486/Disulfide bonds: interchain (to IgA alpha-1 chain-192) #status experimental

F;520/Binding site: cysteine (Cys) (covalent) (in Ig-bound form) #status experimental

F;577-578/Cleavage site: Lys-Ala (unidentified proteinase) #status experimental

F;673/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 9.0%; Score 134.5; DB 1; Length 764;

Best Local Similarity 25.3%; Pred. NO. 0.0032;

Matches 64; Conservative 31; Mismatches 109; Indels 49; Gaps 9;

Qy 1 MPLLLYLLFWLSCYSTATQITGTTVNGLESGSLTVQCVY--RSGWETYLKWKCRGAI 58

Db 1 MLFVLTCLLAVFPAISKSPITGFPEEVSNGSVSICYYPTFSVNRHTRKYWCROGA 60

Qy 59 WRDCKILVKTSGEQEVRDRVISKDNKNRTFTVTMDLTKTDADTYWC--GIEKTGND 116

Db 61 RGCCITLISSEGVSSKYAGRANLTFPENGTFVNVIAQLSQDDSGRYKCGLGINSRGLS 120

Qy 117 LGVTQVITDPAVPTQEE-----TSSSPPTTGHLDNRHKLKLSVLPLIF--- 163

Db 121 FDVSLVSGQGLLNDTKVYTVDLGRVTINCPFKT-ENAQKRKSLYKQIGLYPLVIDS 179

Qy 164 -----TIXLLLVAAASLLAWRMW---KYQQAAGMSPE-----QV 195

Db 180 SGVYVNPYTGRIELDIQGTGQLLFVSVINQL--RLSDAGYLCOAGDDSNKKNADLQV 237

Qy 196 LQPLEGDLCYADL 208

Db 238 LXP-EPELVYEDL 249

RESULT 6

S48841

secretory component precursor - bovine

N;Alternate names: poly-Ig receptor; polymeric immunoglobulin receptor

K;Contains: free secretory component; transmembrane secretory component

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999

C;Accession: S48841

R;Vermeer, H.; Warmerdam, G.W.; de Boer, H.A.; Verbeet, M.P.H. submitted to the EMBL Data Library, September 1994

A;Description: The cloning, tissue specific expression and interspecies sequence compari

A:Reference number: S48841
A:Accession: S48841
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-757 <VER>
A:Cross-references: EMBL:X81371; NID:G563340; PIDN:CAA57136.1; PID:G563341
C:Superfamily: secretory component; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin receptor; phosphoprotein; transcytosis
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-572/Product: transmembrane secretory component #status predicted <MAT>
F:19-572/Product: free secretory component #status predicted <MAT>
F:33-112/Domain: immunoglobulin homology <IM1>
F:145-223/Domain: immunoglobulin homology <IM2>
F:250-328/Domain: immunoglobulin homology <IM3>
F:368-444/Domain: immunoglobulin homology <IM4>
F:476-547/Domain: immunoglobulin homology <IM5>
F:631-653/Domain: transmembrane #status predicted <TM>
F:654-757/Domain: intracellular #status predicted <INT>
F:40-110,56-64,152-220,166-173,257-324,271-279,370-440,384-394,481-543,495-502/Disulfide
F:83,420,468/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:665/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 8.8%; Score 132.5; DB 1; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.0046;
Matches 59; Conservative 40; Mismatches 95; Indels 69; Gaps 8;

QY 1 MRLTLVLLFWLSGYSSTATITGPTTVNGLERGSLTVQCVY--RSGWEYLYKWCRCGAI 58
DB 1 MSRLFLACLLAIFPVVSMKSPFPGPEVSVEGSRVSIKCYPPPTSVNRHTRKWCRCQA 60

QY 59 WRDCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWC--GIEKTGND 116
DB 61 QQRCTTLISSEGYSDVDVGRANLTNPFESGTFVVDISHLTHKDSGRYKCOLGISRRGLN 120

QY 117 LGVTQVQVITDPA-----PVQETSSSPTL-----T 142
DB 121 FDSVLEVSQDPAQASHAHVYTDLGRVTINCPTFRANSEKRSKSLCKKTIQDQCFQVVDST 180

QY 191 -----SPEQVLOPLEGDLCLYADL 208
DB 228 ADKINIDQLVLEP-EPELVYGD 249

RESULT 7
I45956
polymeric immunoglobulin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 23-Jul-1999
C:Accession: I45956
A:Title: Cloning and characterization of two forms of bovine polymeric immunoglobulin re
A:Reference number: I45956; MUID:95186063; PMID:7880445
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-757 <KUL>
A:Cross-references: GB:LO4797; NID:G388279; PIDN:AA41620.1; PID:G388280
C:Superfamily: secretory component; immunoglobulin homology
F:145-222/Domain: immunoglobulin homology <IM>

Query Match 8.8%; Score 131.5; DB 2; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.0056;
Matches 59; Conservative 39; Mismatches 96; Indels 69; Gaps 8;

QY 1 MRLTLVLLFWLSGYSSTATITGPTTVNGLERGSLTVQCVY--RSGWEYLYKWCRCGAI 58
DB 1 MSRLFLACLLAIFPVVSMKSPFPGPEVTSVEGSRVSIKCYPPPTSVNRHTRKWCRCQA 60

QY 59 WRDCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWC--GIEKTGND 116
DB 61 QQRCTTLISSEGYSDVDVGRANLTNPFESGTFVVDISHLTHKDSGRYKCOLGISRRGLN 120

QY 117 LGVTQVQVITDPA-----PVQETSSSPTL-----T 142
DB 121 FDSVLEVSQDPAQASHAHVYTDLGRVTINCPTFRANSEKRSKSLCKKTIQDQCFQVVDST 180

QY 143 GHLDNRHKLKLSVL--LPIFTIXLLVLAASLLAWRMKYYQQAAGM----- 190
DB 181 GYVSNKYKDRAHISILGNTLVFVSVI-----NRVLSADAGMVCQAGDDAK 227

QY 191 -----SPEQVLOPLEGDLCLYADL 208
DB 228 ADKINIDQLVLEP-EPELVYGD 249

RESULT 8
S03421
T-cell receptor delta chain precursor (peer) - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: S03421
R:Joh, E.Y.; Lanier, L.L.; Turck, C.W.; Littman, D.R.; Davis, M.M.; Chien, Y.H.; Weiss, F.
A:Title: Identification and sequence of a fourth human T cell antigen receptor chain.
A:Reference number: S03421; MUID:88065901; PMID:2825032
A:Accession: S03421
A:Molecule type: mRNA
A:Residues: 1-232 <LOH>
A:Cross-references: EMBL:X06557; NID:G37003; PIDN:CAA29800.1; PID:G37004
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-292/Product: T-cell receptor delta chain #status predicted <MAT>

Query Match 8.6%; Score 129.5; DB 2; Length 292;
Best Local Similarity 24.3%; Pred. No. 0.0026;
Matches 35; Conservative 34; Mismatches 64; Indels 11; Gaps 4;

QY 4 LTLVLLFWLSGYSSTATITGPTTVNGLERGSLTVQCVYRSGWEYLYKWCRCGAIMRDC 62
DB 6 LLCVFAFSYSGSSVAQKVQQAQSSVNFVKAVTLCVETSWWSYIFWVKQLPSKEM 65

QY 63 KILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWC-----GIEKTGN 115
DB 66 IFLIRGSDQNAKSGRYSVNFKAAKSVALTISALQLEDSAKYFCALGTGVRGLQDTDK 125

QY 116 DL-GVTQVQVITDPAVTOETSSS 138
DB 126 LIFGKGRVTVBEPR--SQPHTKPS 147

RESULT 9
S04664
T-cell receptor delta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-May-1997
C:Accession: S04664
R:Okada, A.; Bank, I.; Rogozinski, L.; Takihara, Y.; Mak, T.W.; Chess, L.; Alt, F.W.
J. Exp. Med. 168, 1481-1486, 1988
A:Title: Structure of the gamma/delta T cell receptor of a human thymocyte clone.
A:Reference number: S04663; MUID:89010543; PMID:2844954
A:Accession: S04664
A:Molecule type: mRNA
A:Residues: 1-142 <OKA>
A:Cross-references: EMBL:X15021
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 8.6%; Score 128.5; DB 2; Length 142;
Best Local Similarity 24.4%; Pred. No. 0.0013;


```
Matches 32; Conservative 33; Mismatches 59; Indels 7; Gaps 3;
QY 4 LTLVLLFWLSGYSIAQIT-GPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWRDC 62
D 6 LLLCVFAFSYSGSSVAQKVTAQSSVMPVRKAVTLNCLYETSWWSYIIFWYKQLPSKEM 65
QY 63 KILVKTSGSEQVDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGI-----EKTGNDL- 117
D 66 IFLRQSDQNAKSGRYSVNFKAAKSVALTISALQLEDSAKYFCALGHLPTEWGDKLI 125
QY 118 -GVTVQVTIDP 127
D 126 FGKGRVTVEPR--SQPHTRPS 136

RESULT 10
A40131
T-cell receptor delta chain V-J-C regions (JDP2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: A40131
R:Hata, S.; Brenner, M.B.; Krangel, M.S.
Science 236, 678-682, 1997
A>Title: Identification of putative human T cell receptor delta complementary DNA clones
A:Reference number: A40131; MUID:98042795; PMID:3499667
A:Accession: A40131
A:Molecule type: mRNA
A:Residues: 1-293 <HAT>
A:Cross-references: GB:W18414; NID:G339378; PID:AAA61102.1; PID:G339379
A>Note: the reported sequence is a composite from 4 overlapping clones. Differences were
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 8.5%; Score 127.5; DB 2; Length 293;
Best Local Similarity 23.4%; Pred. No. 0.0038;
Matches 34; Conservative 31; Mismatches 61; Indels 19; Gaps 3;
QY 11 FWLSGYSIAQIT-GPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWRDCILVKTSS 69
D 6 FSYSGSSVAQKVTAQSSVMPVRKAVTLNCLYETSWWSYIIFWYKQLPSKEMIFLIROG 65
QY 70 GSEQVDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIETKTGNDL----- 117
D 66 SDEQNAKSGRYSVNFKAAKSVALTISALQLEDSAKYFCALAVRGKLLERNGGYAVFPSPD 125
QY 118 ---GVTVQVTIDPAPVTQBEETSS 138
D 126 KLIFGKGRVTVEPR--SQPHTRPS 148

RESULT 11
S04915
T-cell receptor delta chain precursor V-D-J region (clone KTI0E) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C:Accession: S04915; PL0073
R:Akaiharu, Y.; Reimann, J.; Michalopoulos, E.; Ciccone, E.; Moretta, L.; Mak, T.W.
J. Exp. Med. 169, 393-405, 1989
A>Title: Diversity and structure of human T cell receptor delta chain genes in peripheral
A:Reference number: PL0073; MUID:89094239; PMID:2521355
A:Accession: S04915
A:Molecule type: mRNA
A:Residues: 1-157 <TAK>
A:Cross-references: EMBL:X14545; NID:G37302; PIDN:CAA32681.1; PID:G37303
A>Note: translation of the nucleotide sequence is not complete
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-157/Product: T-cell receptor delta chain (fragment) #status predicted <MAT>
F:22-114/Domain: V region (V-delta-1) <VRE>
F:124-137/Domain: J region (J-delta-1) <JRE>
F:139-157/Domain: C region (fragment) <CRE>
```

```
Query Match 8.5%; Score 127; DB 2; Length 157;
Best Local Similarity 23.1%; Pred. No. 0.002;
Matches 33; Conservative 34; Mismatches 66; Indels 10; Gaps 3;
QY 4 LTLVLLFWLSGYSIAQIT-GPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWRDC 62
D 6 LLLCVFAFSYSGSSVAQKVTAQSSVMPVRKAVTLNCLYETSWWSYIIFWYKQLPSKEM 65
QY 63 KILVKTSGSEQVDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIETKTGND----- 116
D 66 IFLRQSDQNAKSGRYSVNFKAAKSVALTISALQLEDSAKYFCALGEAPSANGKHL 125
QY 117 -LGVTVQVTIDPAPVTQBEETSS 138
D 126 IFGKGRVTVEPR--SQPHTRPS 146

RESULT 12
I46634
rearranged T-cell receptor delta-chain/ Vdelta1.12-Bdeltas-Jdelta1 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46634
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A>Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46634
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-138 <YAN>
A:Cross-references: GB:D49575; NID:G1041152; PID:BAA08519.1; PID:G1041153
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 8.4%; Score 126.5; DB 2; Length 138;
Best Local Similarity 22.5%; Pred. No. 0.0019;
Matches 32; Conservative 31; Mismatches 60; Indels 19; Gaps 4;
QY 1 MPLLTLVLLFWL-----SGYSIAQITGPTTVNGLERG-SLTVQCVYRSGWETYLKWW 53
D 1 MFLSS-----LLWLFASVFGSGVSKVQTPQPVVRQVGEVTLNCHYEISWVHILFW 56
QY 54 CRGAIWRDCILVKTSGSEQVDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIETKT 113
D 57 YKQLENGEMTFLIRODTSKTNAKDDRYSVNRRGKSLTISALQLEDSATYFCALREG 116
QY 114 GND-----LGVTVQVTIDP 127
D 117 GTGTGVYKNLIFGKGTQLVVEP 138

RESULT 13
I46628
rearranged T-cell receptor delta-chain/ Vdelta1.6-Ddeltas-Jdelta1 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46628
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A>Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46628
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-137 <YAN>
A:Cross-references: GB:D49569; NID:G1041140; PIDN:BAA08513.1; PID:G1041141
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 8.4%; Score 126; DB 2; Length 137;
Best Local Similarity 24.8%; Pred. No. 0.002;
Matches 35; Conservative 27; Mismatches 61; Indels 18; Gaps 4;
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QY      1  MPLLTLTLLFL-----SGYSIATQITGPTTNGLGRG-SLTVCQCYRSGWETYLKW 53
Db      1  MPSS-----LLWLFLASVFGSSMAQKVTDQPVVSRQVGEVTLNCRYETSMWEYILFW 56
QY     54  CRGAIVRDKILVKTSSBEVKKDRVISIKDNQKRTFTVTMEDIMKTDADTYNCGETK 113
Db     57  YKQPPSGEMFTLIQRYSITGNNAKEDRYISINFQAKQGISLTISALQMKDSATYFCVLWAT 116
QY    114  GND-----LGVTVQVTIDP 127
Db    117  WTGRWEDKLIFGKGTQLVVEP 137

RESULT 14
I46633
rearranged T-cell receptor delta-chain/ Vdelta1.11-Ddelta5-Jdelta1 - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C/Accession: I46633
R/X: Tang, Y.-G.; Ohtsu, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1991-1993, 1995
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A/Reference number: I46623; MUID:95363165; PMID:7636249
A/Accession: I46633
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-145 <YAN>
A/Cross-references: GB:D49574; NID:g1041150; PIDN:RAA08518.1; PID:g1041151
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

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Db      1  MFLSPLPWLIAFTSGSGVAQKVTDQDSVSSQVGQSVTLSCRYETSSVYVLYWYKOL 60
Qy      58  IWRDCKILVKTSGSEQEVKRDVSIKDNQKNRFTFTMEDLMKTDADTYWCIGIEKTGNDL 117
Db      61  LSGQMTYVIRGSEATNARKERISVNFQAEKSIKLITISALQIGDSAKYFCALSINPLIF 120
Qy      118  GVTQVITDP 127
Db      121  GKGTYLVNEP 130

Search completed: September 16, 2004, 12:40:34
Job time : 42 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:24:14 ; Search time 24 Seconds
(without alignments)

629.181 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 1499

Sequence: 1 WPLTLYLLFWLSGVSIAT.....SKLPGRGPEPTYSISR 290

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224.5	15.0	224	1 CM35_HUMAN	Q08708 homo sapien
2	159.5	10.6	773	1 PIGR_RABIT	P01832 cryptolagus
3	153	10.2	771	1 PIGR_MOUSE	O70570 mus musculus
4	145.5	9.7	769	1 PIGR_RAT	P15083 rattus norv
5	134.5	9.0	764	1 PIGR_HUMAN	P01833 homo sapien
6	131.5	8.8	757	1 PIGR_BOVIN	P81265 bos taurus
7	99	6.6	129	1 KVLW_HUMAN	P04431 homo sapien
8	98.5	6.6	1694	1 SN_MOUSE	Q62230 mus musculus
9	97	6.5	598	1 LIB2_HUMAN	Q8N423 h leukocyte
10	95.5	6.4	102	1 PIGR_PIG	Q29244 sus scrofa
11	92.5	6.2	506	1 SHS1_BOVIN	O46631 bos taurus
12	92.5	6.2	823	1 CEK3_CHICK	P18461 gallus gall
13	92	6.1	134	1 TVAL_RABIT	P06322 cryptolagus
14	92	6.1	249	1 HCDR_XANP2	Q36840 xanthobacte
15	92	6.1	4911	1 MLL3_HUMAN	Q9NEZ4 homo sapien
16	91.5	6.1	457	1 CD4_RAT	P05540 rattus norv
17	91	6.1	117	1 KVLJ_HUMAN	P01602 homo sapien
18	91	6.1	650	1 LIB1_HUMAN	Q9NH16 h leukocyte
19	90	6.0	359	1 LACH_DROME	Q24372 drosophila
20	89.5	6.0	116	1 HVL1_HUMAN	P03983 heterodontu
21	88	5.9	1176	1 KML5_BOVIN	Q28824 bos taurus
22	88	5.9	4391	1 PGBM_HUMAN	P98160 homo sapien
23	87	5.8	519	1 TRPE_BUCDN	Q94697 buthnera ap
24	86.5	5.8	284	1 HXRD_HETFR	Q91A17 heterodontu
25	86.5	5.8	821	1 FGR2_MOUSE	P12803 mus musculus
26	86	5.7	1141	1 CN3A_HUMAN	P14432 homo sapien
27	85.5	5.7	298	1 ERA_XYLET	Q87C05 xyliella fas
28	85.5	5.7	876	1 TOP1_VIBCH	Q9KRB2 vibrio chol
29	85	5.7	131	1 TVAL_HUMAN	P04436 homo sapien
30	85	5.7	3396	1 PGCV_HUMAN	P13611 homo sapien
31	84.5	5.6	448	1 LIB4_HUMAN	Q9NH16 homo sapien
32	84.5	5.6	1808	1 TENA_CHICK	P10039 gallus gall
33	84	5.6	460	1 CT54_MOUSE	Q9D6X5 mus musculus

ALIGNMENTS

RESULT 1

CM35_HUMAN STANDARD; PRT; 224 AA.

AC	Q08708;	5.6	594	1	NLFB_DROME	Q9Y113 drosophila
DT	01-OCT-1996 (Rel. 34, Created)	5.6	120	1	KVZB_MOUSE	P01627 mus musculus
DT	01-OCT-1996 (Rel. 34, Last sequence update)	5.6	132	1	TVAZ_MOUSE	P01739 mus musculus
DT	10-OCT-2003 (Rel. 42, Last annotation update)	5.6	298	1	ERA_XYLFA	Q9PB97 xyliella fas
DE	CMRF35 antigen precursor (CMRF-35).	5.6	503	1	SHS1_HUMAN	P78324 h protein-t
GN	CMRF35 OR CMRF35A.	5.6	509	1	SHS1_RAT	P97710 x protein-t
OS	Homo sapiens (Human).	5.5	110	1	KVL1_RABIT	P01682 cryptolagus
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	5.5	438	1	HVC2_HETFR	P23085 heterodontu
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.	5.5	776	1	GCR_TUPGB	Q95267 tupaiia glis
OX	NCBI_TaxID=9606;	5.5	1256	1	FINC_CHICK	P11722 gallus gall
RN	[1]	5.5	457	1	CD4_SAISC	Q29037 saimiri sci
RP	SEQUENCE FROM N.A.	5.5	595	1	SIL1_HUMAN	Q96PQ1 homo sapien
RX	MEDLINE=2249405; PubMed=1349532;					
RA	Jackson D.G., Hart D.N.J., Starling G., Bell J.I.;					
RT	"Molecular cloning of a novel member of the immunoglobulin gene					
RT	superfamily homologous to the polymeric immunoglobulin receptor.";					
RL	Eur. J. Immunol. 22:1157-1163(1992).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=21442079; PubMed=11556966;					
RA	Clark G.J., Cooper B., Fitzpatrick S., Green B.J., Hart D.N.;					
RT	"The gene encoding the immunoregulatory signaling molecule CMRF-35A					
RT	localized to human chromosome 17 in close proximity to other members					
RT	of the CMRF-35 family.";					
RL	Tissue Antigens 57:415-423(2001).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lung;					
RX	MEDLINE=22388257; PubMed=12477932;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,					
RA	Brownstein R.W., Uddin T.B., Toshitoki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,					
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length					
RT	human and mouse cDNA sequences.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (potential).					
CC	-1- TISSUE SPECIFICITY: PRESENT ON THE SURFACE OF MONOCYTES,					
CC	NEUTROPHILS, A PROPORTION OF PERIPHERAL BLOOD T AND B LYMPHOCYTES					
CC	AND LYMPHOCYTIC CELL LINES.					

QY 53 WCGAIWRDCKILVKTSGSQEVRKDRVSIKDNQKNTFTVTWEDLMKTDADTYWCGIEK 112
 DB 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDPDGFEVTVTDQNDGSGYKCGVG 119
 QY 113 TGN--DAGVTVQVTDAP---VTOBETSSPILTGHLNDRHKLKLSVLLPLIFTI-- 165
 DB 120 NGRGLDGVNVLVSQKEPDVVKQVESVTVITCPFTVATQQLK-----SFYKVED 173
 QY 166 -XLILLVAALLAWRMKMYQKQAGMSPEQVLOFLEGDLACYADLTQLAGTSRKAATKL 224
 DB 174 GELVLIIDSSSKAKDPYKGR-----ITLIQISTTAKEFTVTI 212
 QY 225 SSAQVDQVEVEYVMA-----SLPEDISYASLILGAEDQFTYCNMG 267
 DB 213 KHLQLNDAG-QYVCQSGSDPTAEQNVDLRLLPGL-----LYGNLG 253

RESULT 3
 PIGR MOUSE
 ID PIGR MOUSE STANDARD; PRT; 771 AA.
 AC O70570;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Polymorphic-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
 DE [Contains: Secretory component].
 GN PIGR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
 RX MEDLINE=95138517; PubMed=7836758;
 RA Piskurich J.F., Blanchard M.H., Youngman K.R., France J.A.,
 RA Kaetzel C.S.;
 RT "Molecular cloning of the mouse polymeric Ig receptor. Functional
 RT regions of the molecule are conserved among five mammalian species.";
 RL J Immunol. 154:1735-1747(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98072444; PubMed=9409786;
 RA Martin M.G., Gutierrez E.M., Lam J.T., Li T.W.H., Wang J.;
 RT "Genomic cloning and structural analysis of the murine polymeric
 RT receptor (p19R) gene and promoter region.";
 RL Gene 201:189-197(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Liver;
 RX MEDLINE=99410926; PubMed=10481312;
 RA de Groot N., van Kuik-Romeijn P., Lee S.H., de Boer H.A.;
 RT "Over-expression of the murine polymeric immunoglobulin receptor gene
 RT in the mammary gland of transgenic mice.";
 RL Transgenic Res. 8:125-135(1999).
 CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
 CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
 CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
 CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
 CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
 CC TRANSMEMBRANE SEGMENT (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
 CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
 CC
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 CC -----

DR EMBL; U06431; AA67440.1; -.
 DR EMBL; U83434; AAC53585.1; -.
 DR EMBL; U83427; AAC53585.1; JOINED.
 DR EMBL; U83428; AAC53585.1; JOINED.
 DR EMBL; U83429; AAC53585.1; JOINED.
 DR EMBL; U83430; AAC53585.1; JOINED.
 DR EMBL; U83431; AAC53585.1; JOINED.
 DR EMBL; U83432; AAC53585.1; JOINED.
 DR EMBL; U83433; AAC53585.1; JOINED.
 DR EMBL; U83434; AAC53585.1; JOINED.
 DR EMBL; U16524; CAA76272.1; -.
 DR EMBL; U16525; CAA76272.1; JOINED.
 DR EMBL; U16526; CAA76272.1; JOINED.
 DR EMBL; U16527; CAA76272.1; JOINED.
 DR EMBL; U16528; CAA76272.1; JOINED.
 DR EMBL; U16529; CAA76272.1; JOINED.
 DR EMBL; U16530; CAA76272.1; JOINED.
 DR EMBL; U16531; CAA76272.1; JOINED.
 DR EMBL; U16532; CAA76272.1; JOINED.
 DR MGD; MGI:103080; Pigr.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00409; IG; 3.
 DR PROSITE; PS00835; IG LIKE; 3.
 KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 771
 FT CHAIN 19 611
 FT DOMAIN 19 645
 FT TRANSMEM 646 668
 FT DOMAIN 669 771
 FT DOMAIN 21 120
 FT DOMAIN 135 237
 FT DOMAIN 245 351
 FT DOMAIN 352 457
 FT DOMAIN 463 563
 FT DISULFID 40 110
 FT DISULFID 152 220
 FT DISULFID 257 324
 FT DISULFID 370 440
 FT DISULFID 484 546
 FT CARBOHYD 90 90
 FT CARBOHYD 147 147
 FT CARBOHYD 170 170
 FT CARBOHYD 206 206
 FT CARBOHYD 420 420
 FT CARBOHYD 471 471
 FT CONFLICT 159 159
 FT CONFLICT 396 396
 FT CONFLICT 620 620
 FT SEQUENCE 771 AA; 84998 MW; 78C81302EC710730 CRC64;
 Query Match 10.2%; Score 153; DB 1; Length 771;
 Best Local Similarity 22.4%; Pred. No. 7.3e-06;
 Matches 76; Conservative 46; Mismatches 144; Indels 74; Gaps 12;
 QY 3 LITLLXLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYL-----KWCRCGA 57
 DB 5 LFTLLVTVF--SGVSTKSPIFGPQSVSSIEGDSVSICTYCP--DTSVNRHTRKYWCROG 59
 QY 58 IWRDCKILVKTSQGEVVRKDRVSIKDNQKRTFTVTWEDLMKTDADTYWCGIEKTGNDL 117
 DB 60 ASGMCTTLLISSNGYLSKEYSGRANLINFENNFTVINIEQJTDQDTGSKGCLGTSNRGL 119
 QY 118 GYTVQVTTDPAP-----VTOB-----ETSSSPILTIGHH 145
 DB 120 SFDVSLVSQVPELPSDTHVTKDIGRNVITIECPKRENAPSKSLCKKTNQSCELV--- 176
 QY 146 LDRHKLKLSVLLPLIF---TIXLLLVAAALLAWRMKMYQKQAGMSPE-----Q 194
 DB 177 IDSTEKVPSTYGRAKLFMKGTDLTVFYVNIHSLTHNDAGLYICQAGEGPSADKKNVDLQ 236
 QY 195 VLPQLEGDLYADLTQLA-----QTSPRKATTKLSSAQVDQVEVEYVMA----- 241

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Db 237 VLAP-EPALLYKDLRSSVTFSCDLGREVANEAKYLCRMNKETCDVIINTLGRKDPDFEGR 295
QY 242 ---LPKEDIS-YASLTLAGEDQETTCYCMGXLSSXLPGRG 277
Db 296 ILITPKDNGRFRSLITGLRKEDAGHYCCGAHSSGLPQEG 335

RESULT 4
PIGR_HUMAN
ID PIGR_HUMAN STANDARD; PRT; 769 AA.
AC P15083;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
DE [Contains: Secretory component].
GN PIGR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89378226; PubMed=2776882;
RA Banting G., Brake B., Braghetta P., Luzio J.P., Stanley K.K.;
RT "Intracellular targeting signals of polymeric immunoglobulin
RL FEBS Lett. 254:177-183(1989).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
CC TRANSMEMBRANE SEGMENT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X15741; CAA33758.1; -.
CC PIR; S05407; QRRGTS.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003599; IG.
CC DR Pfam; PF00047; Ig_5.
CC DR SMART; SM00409; IG_5.
CC DR PROSITE; PS00835; IG LIKE; 2.
CC KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal.
CC SIGNAL
CC CHAIN 1 18 POLYMERIC-IMMUNOGLOBULIN RECEPTOR.
CC FT CHAIN 19 769 SECRETORY COMPONENT.
CC FT CHAIN 19 611 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 19 643 POTENTIAL.
CC FT TRANSMEM 644 666 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 667 769 IG-LIKE V-TYPE 1.
CC FT DOMAIN 21 126 IG-LIKE V-TYPE 2.
CC FT DOMAIN 135 237 IG-LIKE V-TYPE 3.
CC FT DOMAIN 240 341 IG-LIKE V-TYPE 4.
CC FT DOMAIN 353 457 IG-LIKE V-TYPE 5.
CC FT DOMAIN 463 563 POTENTIAL.
CC FT DISULFID 40 110 POTENTIAL.
CC FT DISULFID 152 220 POTENTIAL.
CC FT DISULFID 257 324 POTENTIAL.
CC FT DISULFID 370 440 POTENTIAL.
CC FT DISULFID 484 546 POTENTIAL.
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 769 AA; 84798 MW; 5F849303400255A7 CRC64;
Query Match 9.7%; Score 145.5; DB 1; Length 769;
Best Local Similarity 21.4%; Pred. No. 3.5e-05;
Matches 74; Conservative 51; Mismatches 137; Indels 83; Gaps 13;
QY 4 LTLVLLFWL-SGYSIATQITGTTVNGLSGLTVQCVYRSGMETYL-----KWWCRGA 57
Db 3 LSLFALLVTVFSGVSTQSPIFGPQDVSSIEGNSVITCYP--DTSVNRHTRKYWCRCQ 59
QY 58 IWRDCKILVKTSGSQEYKRVDSIKDKQKRTFTVTMEDLMKTDADTYWGIEKTGNDL 117
Db 60 ANGYCATLISNGYLSKEYSGRASLINFENSTFVINIAHLTQEDTSGYKCGLTNRGL 119
QY 118 GVTVOVTIDPAPVTOET-----SSPTL-----T 142
Db 120 FFDVLSVQVPEFNDTHVYTKDIGRTVTIECRFEGNAHSKSLCKKRGCEAVVIDS 179
QY 143 GHLDNRHK---LLKSLVLLPLFTIXLLLLVA--ASLLAWMMKYQOKAAGMSPE---- 193
Db 180 TEYVDPYSKDRALFEMKGTSRDIFYVNIHSLIPSDAGLYVCQ-----AGEGFSADKN 231
QY 194 ----OVLOPLEGLDLCYADITLQLA-----GTSPRKATTKLSSAQVDQVEVVTWAS--- 241
Db 232 NADLQVLEP-EPALLYKDLRSSVTFECDLGREVANDAKYLCKNKETCDVIINTLGRKDP 290
QY 242 -----LPKEDIS-YASLTLAGEDQETTCYCMGXLSSXLPGRG 277
Db 291 AFEGRILLTFRDNGRFRSLITGLRKEDAGHYCCGAHSSGLPQEG 335

RESULT 5
PIGR_HUMAN
ID PIGR_HUMAN STANDARD; PRT; 764 AA.
AC P01833;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor precursor (Poly-Ig receptor) (PIGR)
DE [Contains: Secretory component].
GN PIGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92039621; PubMed=1682231;
RA Krajci P., Grzeschik K.H., Geurts van Kessel A.H., Olaisen B.,
RA Brandtzaeg P.;
RT "The human transmembrane secretory component (poly-Ig receptor);
RT molecular cloning, restriction fragment length polymorphism and
RT chromosomal sublocalization.";
RL Hum. Genet. 87:642-648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92387236; PubMed=1355431;
RA Krajci P., Kvale D., Tasken K., Brandtzaeg P.;
RT "Molecular cloning and exon-intron mapping of the gene encoding human
RT transmembrane secretory component (the poly-Ig receptor).";
RL Eur. J. Immunol. 22:2309-2315(1992).
RN [3]
RP SEQUENCE OF 72-764 FROM N.A.
RX MEDLINE=89149795; PubMed=2920039;
RA Krajci P., Solberg R., Sandberg M., Oyen O., Jahnsen T.,
RA Brandtzaeg P.;
RT "Molecular cloning of the human transmembrane secretory component
RT (poly-Ig receptor) and its mRNA expression in human tissues.";
RL Biochem. Biophys. Res. Commun. 158:783-789(1989).
RN [4]
RP SEQUENCE OF 19-577, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

```

RX MEDLINE=95128981; PubMed=6526384;
RA Eifert H., Quentin E., Decker J., Hillemeir S., Hufschmidt M.,
PA Klingmüller D., Weber M.H., Hilschmann N.;
PT "The primary structure of human free secretory component and the
RT arrangement of disulfide bonds.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1489-1495 (1984).
RN [5]
RP SEQUENCE OF 19-577.
RX MEDLINE=91315750; PubMed=1859628;
RA Eifert H., Quentin E., Wiederhold M., Hillemeir S., Decker J.,
PA Weber M., Hilschmann N.;
PT "Determination of the molecular structure of the human free secretory
RT component.";
RL Biol. Chem. Hoppe-Seyler 372:119-128 (1991).
RN [6]
RP SEQUENCE OF 118-138; 212-230; 232-268; 273-288 AND 578-603.
RX MEDLINE=97379357; PubMed=9237679;
RA Hughes G.J., Frutiger S., Savoy L.-A., Reason A.J., Morris H.R.,
PA Jaton J.-C.;
PT "Human free secretory component is composed of the first 595 amino
RT acid residues of the polymeric immunoglobulin receptor.";
RL FEBS Lett. 410:443-446 (1997).
RN [7]
RP -1- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
CC EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
CC TRANSMEMBRANE SEGMENT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -1- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
CC -----
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CC -----
DR EMBL; S62403; AAB20203.1; -;
DR EMBL; S43449; AAB23176.1; -;
DR EMBL; S43437; AAB23176.1; JOINED.
DR EMBL; S43441; AAB23176.1; JOINED.
DR EMBL; S43442; AAB23176.1; JOINED.
DR EMBL; S43443; AAB23176.1; JOINED.
DR EMBL; S43444; AAB23176.1; JOINED.
DR EMBL; S43445; AAB23176.1; JOINED.
DR EMBL; S43446; AAB23176.1; JOINED.
DR EMBL; S43447; AAB23176.1; JOINED.
DR EMBL; S43448; AAB23176.1; JOINED.
DR EMBL; M24559; AAB36102.1; -;
DR EMBL; A52091; CAA03384.1; -;
DR PIR; A46537; ORHUGS.
DR GlycoSuiteDB; P01833; -;
DR Genew; HGNC:8968; FIGR.
DR MIW; 173880; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 5.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal;
KW Polymorphism.
FT SIGNAL 1 18
FT CHAIN 19 764
FT CHAIN 19 603
FT DOMAIN 19 638
FT TRANSMEM 639 661
FT DOMAIN 662 764
FT DOMAIN 19 120
FT DOMAIN 145 237
FT DOMAIN 250 352
FT IG-LIKE V-TYPE 3.

FT DOMAIN 364 458
FT DOMAIN 462 561
FT DISULFID 40 110
FT DISULFID 56 64
FT DISULFID 152 220
FT DISULFID 257 325
FT DISULFID 271 279
FT DISULFID 371 441
FT DISULFID 385 395
FT DISULFID 482 544
FT DISULFID 486 520
FT DISULFID 496 503
FT CARBOHYD 83 83
FT CARBOHYD 90 90
FT CARBOHYD 135 135
FT CARBOHYD 186 186
FT CARBOHYD 421 421
FT CARBOHYD 469 469
FT CARBOHYD 499 499
FT VARIANT 580 580
FT CONFLICT 136 136
FT CONFLICT 158 158
FT CONFLICT 208 209
FT CONFLICT 229 229
FT CONFLICT 234 234
FT CONFLICT 241 241
FT CONFLICT 262 262
FT CONFLICT 280 280
FT CONFLICT 392 392
FT CONFLICT 500 500
SQ SEQUENCE 764 AA; 83313 MW; 916B3B662C339950 CRC64;
Query Match 9.0%; Score 134.5; DB 1; Length 764;
Best Local Similarity 25.3%; Pred. No. 0.00034;
Matches 64; Conservative 31; Mismatches 109; Indels 49; Gaps 9;
QY 1 MPELLLYLLFWLSGYSIATQITGPTTVNGLESGSLTVQCVY--RSGWETVYKWCRCGAI 58
DB 1 MLFVLTCLLAVFPFAISTKSPFGPEEVNVEGNSVITCYPPPTSVNRHTRKYWCRCGA 60
QY 59 WRDCKILVKTSGEQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWC--GIBKTGND 116
DB 61 RGGCITLISSEGYVSSKAGRANLTNFPENGTFVFNIAQLSQDDSGRYKCGLGINSRGLS 120
QY 117 LGVTQVQIDPAPVTQEE-----TSSSPITLTHLDRHKLKLLVLLPLIF--- 163
DB 121 FDSVLEVSQGPGLNDTKVYTVDLGRVTINCPFKT--ENAKRKSLYKQIGLYPLVIDS 179
QY 164 -----TIXLLLVAAALLAWRMW---KYQKKAAGMSPE-----QV 195
DB 180 SGVYNPNTGRIRLDIQGTGQLLPSVINQL--RLSDAGQVLCQAGDDSNKKNADLQV 237
QY 196 LQPLEGDLICYADL 208
DB 238 LXP-EPELVYEDL 249
RESULT 6
FIGR_BOVIN
ID FIGR_BOVIN STANDARD; PRT; 757 AA.
AC P81265;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polymeric-immunoglobulin receptor precursor (Poly-Ig receptor) (FIGR)
DE [Contains: Secretory component].
DE FIGR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Mammary gland, and Small intestine;
RX MEDLINE=95186063; PubMed=7880445;
RA Kulseth M.A., Krajci P., Myklebust O., Rogne S.;
RT "Cloning and characterization of two forms of bovine polymeric
immunoglobulin receptor cDNA.";
RL DNA Cell Biol. 14:251-256(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96069604; PubMed=7590352;
RA Verbeet M.P., Vermeer H., Warner G.C., de Boer H.A., Lee S.H.;
RT "Cloning and characterization of the bovine polymeric immunoglobulin
receptor-encoding cDNA.";
RL Gene 164:329-333(1995).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE
EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE
TRANSMEMBRANE SEGMENT.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein. Also secreted.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long; Sequence=Displayed;
isoId=P81265-1; Sequence=Displayed;
Name=Short;
isoId=P81265-2; Sequence=VSP 002547;
CC -!- TISSUE SPECIFICITY: FOUND IN MAMMARY GLAND, JEJUNUM, LUNG, KIDNEY
AND SMALL INTESTINE.
CC -!- PTM: IN THE ABSENCE OF DIMERIC IGA, SER-727 IS PHOSPHORYLATED
WHICH ALLOWS PIGR TO FUNCTION NORMALLY
CC -!- SIMILARITY: Contains 5 immunoglobulin-like V-type domains.
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EMBL; L04797; AAC41620.1; -;
DR EMBL; X81371; CAA57136.1; -;
DR PIR; I45956; I45956;
DR PIR; S48841; S48841.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 3.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal;
KW Polymorphism; Phosphorylation; Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 757 POLYMERIC-IMMUNOGLOBULIN RECEPTOR.
FT CHAIN 19 599 SECRETORY COMPONENT (BY SIMILARITY).
FT DOMAIN 19 632 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 633 653 POTENTIAL.
FT DOMAIN 654 757 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 19 126 IG-LIKE V-TYPE 1.
FT DOMAIN 145 237 IG-LIKE V-TYPE 2.
FT DOMAIN 250 341 IG-LIKE V-TYPE 3.
FT DOMAIN 353 457 IG-LIKE V-TYPE 4.
FT DOMAIN 461 560 IG-LIKE V-TYPE 5.
FT DISULFID 40 110 BY SIMILARITY.
FT DISULFID 56 64 BY SIMILARITY.
FT DISULFID 152 220 BY SIMILARITY.
FT DISULFID 257 324 BY SIMILARITY.
FT DISULFID 271 279 BY SIMILARITY.
FT DISULFID 370 440 BY SIMILARITY.
FT DISULFID 384 394 BY SIMILARITY.
FT DISULFID 481 543 BY SIMILARITY.

FT DISULFID 485 519 BY SIMILARITY.
FT DISULFID 495 502 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD RES 727 727 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPLIC 129 346 Missing (in isoform Short).
FT VARIANT 29 29 /FTIG-VSP_002547.
FT VARIANT 142 142 T -> S.
FT VARIANT 404 404 V -> I.
FT VARIANT 413 413 I -> M.
FT VARIANT 435 435 A -> V.
FT VARIANT 435 435 T -> A.
SQ SEQUENCE 757 AA; 82434 MW; DCED67FDD6A5B6C6 CRC64;
Query Match 8.8%; Score 131.5; DB 1; Length 757;
Best Local Similarity 22.4%; Pred. No. 0.00063;
Matches 59; Conservative 39; Mismatches 96; Indels 69; Gaps 8;
QY 1 MELLTYLLFWLSGYSTATQITGTTVNGLERGSLTVQCVY--RSGWETLYKWCRCGAI 58
Db 1 MSRLFLACLLAIFPVVSMKSPIFGPEEVTSGRVSVCIKYPPTSVNRHTRKMKYCRGGA 60
QY 59 WRDCIKLVKTSGEQEVKRDVRSIKDNQNRITFTVMTEDLMKTDADTYWC--GIEKTDND 116
Db 61 QGRCTTLISSEGVSDDYVGRANLNFPESTGFVVDISHLTHKDSGRYKCGLGISRGIN 120
QY 117 LGVTQVTTIDPA-----PVTQETSSPTL-----T 142
Db 121 FDSLEVSQDPAQASHAHVYVDLGRVTINCPFFTRANSEKRSCKKTIQDCFOVDST 180
QY 143 GHLDNRHKLKLSVL--LPLIFTXLLLLVAASLLAWRMKYOQKAAGM----- 190
Db 181 GYVSNKYDRAHISILGINTLVFVSVI-----NRVKLSDAGMYVQAGDDAK 227
QY 191 -----SPEQVLOPLEGDI CYADL 208
Db 228 ADKINIDLVLEP-EPPELVYGD 249
RESULT 7
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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EMBL; X00965; CAA25477.1; ALT_TERM.
DR FIR; A01883; KIHUMK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 111 119 FRAMEWORK-4.
FT DOMAIN 120 129 BY SIMILARITY.
FT DISULFID 45 110
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 5.6%; Score 99; DB 1; Length 129;
Best Local Similarity 27.5%; Pred. No. 0.054;
Matches 30; Conservative 19; Mismatches 56; Indels 4; Gaps 3;

QY 1 MLLTLVLLFWLGLSGYSIATQIT-GPTTVNGLERGSLTVQCVYRSGWETVYKWCRAIW 59
D5 5 VPAQLGLLLWLRGARDICQMTQSPSLASVGVDRVTITCRASQISNLYNWY-QQKPG 63

QY 60 RDCILVKTSGSEGEVKKRDRVSIKDNKRNRTFTVTMDLMKMTDATTWC 108
D5 64 KAPKLLIYAAGSLQSGVTSRFS--GSGSGTDTLTITSSLOPDSATVYC 110

RESULT 8
SN_MOUSE
ID SN_MOUSE STANDARD; PRT; 1694 AA.
AC Q62230; OS5216; Q62228; Q62229;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialoadhesin precursor (Sialic acid binding Ig-like lectin-1) (Siglec-
DE 1) (Sheep erythrocyte receptor) (SER).
GN SN OR SA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Macrophage;
RX MEDLINE=9500950; PubMed=7925291;
RA Crocker P.R., Mucklow S., Boukson V., McWilliam A., Willis A.C.,
RA Gordon S., Milon G., Kelm S., Bradfield P.;
RT "Sialoadhesin, a macrophage sialic acid binding receptor for
RT haemopoietic cells with 17 immunoglobulin-like domains.";
RN EMBO J. 13:4490-4503(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98051930; PubMed=9383289;
RA Mucklow S., Gordon S., Crocker P.R.;
RT "Characterization of the mouse sialoadhesin gene, Sn.";
RL Mamm. Genome 8:934-937(1997).
RN [3]
RP CHARACTERIZATION.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=91266893; PubMed=2050106;
RA Crocker P.R.;
RT "Purification and properties of sialoadhesin, a sialic acid-binding
RT receptor of murine tissue macrophages.";
RL EMBO J. 10:1661-1669(1991).
RN [4]
RP SIALIC ACID BINDING.
RX MEDLINE=95179521; PubMed=7533044;

RA Kelm S., Pelz A., Schauer R., Filbin M.T., Tang S., de Bellard M.E.,
RA Schnaar R.L., Mahoney J.A., Hartnell A., Bradfield P., Crocker P.R.;
RT "Sialoadhesin, myelin-associated glycoprotein and CD22 define a new
RT family of sialic acid-dependent adhesion molecules of the
RT immunoglobulin superfamily.";
RL Curr. Biol. 4:965-972(1994).
RN [5]
RP BINDING TO SPN.
RX MEDLINE=21136329; PubMed=11238599;
RA van den Berg T.K., Nath D., Ziltener H.J., Vestweber D., Fukuda M.,
RA van Die I., Crocker P.R.;
RT "CD43 functions as a T cell counterreceptor for the macrophage
RT adhesion receptor sialoadhesin (Siglec-1).";
RL J. Immunol. 166:3637-3640(2001).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 20-138.
RX MEDLINE=98325385; PubMed=9660955;
RA May A.P., Robinson R.C., Vinson M., Crocker P.R., Jones E.Y.;
RT "Crystal structure of the N-terminal domain of sialoadhesin in
RT complex with 3' sialyllactose at 1.85 A resolution.";
RL Mol. Cell 1:719-728(1998).
RN [7]
RP STRUCTURE OF 20-138 BY NMR, AND MUTAGENESIS OF TRP-21 AND ARG-116.
RX MEDLINE=99321481; PubMed=10393093;
RA Crocker P.R., Vinson M., Kelm S., Drickamer K.;
RT "Molecular analysis of sialoside binding to sialoadhesin by NMR and
RT site-directed mutagenesis.";
RL Biochem. J. 341:355-361(1999).
CC -!- FUNCTION: Macrophage-restricted adhesion molecule that mediates
CC sialic-acid dependent binding to lymphocytes, including
CC granulocytes, monocytes, natural killer cells, B-cells and CD8 T-
CC cells (by similarity). Preferentially binds to alpha2,3-linked
CC sialic acid. Binds to SPN/CD43 on T-cells. May play a role in
CC hemopoiesis.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
CC soluble (isoforms 2 and 3).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q62230-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q62230-2; Sequence=VSP_002573, VSP_002574;
CC Name=3;
CC IsoId=Q62230-3; Sequence=VSP_002575, VSP_002576;
CC -!- TISSUE SPECIFICITY: Expressed by macrophages in various tissues.
CC Highest expression in spleen and lymph node with lower amounts in
CC lung, liver, bone marrow, heart and skin. No expression in thymus,
CC kidney, brain or small intestine.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 16 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; Z36293; CAA85280.1; -;
DR EMBL; Z36233; CAA85288.1; -;
DR EMBL; Z36234; CAA85269.1; -;
DR EMBL; U92842; AAB95641.1; -;
DR EMBL; U92833; AAB95641.1; JOINED.
DR EMBL; U92834; AAB95641.1; JOINED.
DR EMBL; U92836; AAB95641.1; JOINED.
DR EMBL; U92837; AAB95641.1; JOINED.
DR EMBL; U92838; AAB95641.1; JOINED.
DR EMBL; U92839; AAB95641.1; JOINED.
DR EMBL; U92840; AAB95641.1; JOINED.
DR EMBL; U92841; AAB95641.1; JOINED.

DR PIR; S50065; S50065.
 DR PDB; 1QFO; 16-APR-99.
 DR PDB; 1QFP; 16-APR-99.
 DR MGD; MGI:96668; Sn.
 DR GO; GO:0016021; C: integral to membrane; ISS.
 DR GO; GO:0005529; F: sugar binding; ISS.
 DR GO; GO:0016337; P: cell-cell adhesion; ISS.
 DR GO; GO:0007160; P: cell-matrix adhesion; ISS.
 DR GO; GO:0006954; P: inflammatory response; ISS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 16.
 DR SMART; SM00408; IGC2; 5.
 DR PROSITE; PS0835; IG_LIKE; 14.
 DR PROSITE; PS0290; IG_MHC; 1.
 KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
 Immunoglobulin domain; Repeat; Alternative splicing; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 1694
 FT DOMAIN 20 1638
 FT TRANSMEM 1639 1659
 FT DOMAIN 1660 1694
 FT DOMAIN 20 136
 FT DOMAIN 153 235
 FT DOMAIN 239 321
 FT DOMAIN 326 406
 FT DOMAIN 416 508
 FT DOMAIN 509 594
 FT DOMAIN 602 701
 FT DOMAIN 704 781
 FT DOMAIN 795 890
 FT DOMAIN 894 972
 FT DOMAIN 979 1078
 FT DOMAIN 1080 1160
 FT DOMAIN 1171 1263
 FT DOMAIN 1244 1336
 FT DOMAIN 1341 1438
 FT DOMAIN 1441 1519
 FT DOMAIN 1533 1626
 FT SITE 827 829
 FT DISULFID 36 166
 FT DISULFID 41 98
 FT DISULFID 160 218
 FT DISULFID 263 306
 FT DISULFID 347 391
 FT DISULFID 434 492
 FT DISULFID 532 576
 FT DISULFID 625 685
 FT DISULFID 725 770
 FT DISULFID 813 872
 FT DISULFID 911 955
 FT DISULFID 1000 1062
 FT DISULFID 1102 1144
 FT DISULFID 1188 1236
 FT DISULFID 1276 1319
 FT DISULFID 1362 1421
 FT DISULFID 1462 1508
 FT DISULFID 1551 1610
 FT CARBOHYD 159 159
 FT CARBOHYD 266 266
 FT CARBOHYD 299 299
 FT CARBOHYD 340 340
 FT CARBOHYD 500 500
 FT CARBOHYD 583 583
 FT CARBOHYD 693 693
 FT CARBOHYD 722 722
 FT CARBOHYD 737 737
 FT CARBOHYD 882 882
 FT CARBOHYD 1089 1089
 FT CARBOHYD 1099 1099
 FT CARBOHYD 1246 1246
 FT CARBOHYD 1459 1459

FT CARBOHYD 1473 1473
 FT VARSPIC 326 340
 FT
 FT VARSPIC 341 1694
 FT VARSPIC 1528 1598
 FT
 FT VARSPIC 1599 1694
 FT
 FT MUTAGEN 21 21
 FT MUTAGEN 116 116
 FT MUTAGEN 116 116
 Query Match 6.6%; Score 98.5; DB 1; Length 1694;
 Best Local Similarity 23.2%; Pred. No. 1.7;
 Matches 39; Conservative 22; Mismatches 56; Indels 51; Gaps 8;
 QY 3 LITVLLFWLSGYGIATQ---ITQPTTVNGLGRSLTVQCVYSGWETYLKWCRCG--A 57
 DB 1 MCVLSLLLASVFLSGQTWGVSPKQVGLSGSLIIPCIYSPADVPVS---NGITA 57
 QY 58 IWRDCKILVKTSGSEQEV-----KRDVSIKDNOKNRTFTVTMEDLTKTDADT 105
 DB 58 IW-----YYDSGRQVVIHSGDPKLVDRFRGRAELMGNMDHKVNCNLLKDLKPEDSGT 112
 QY 106 Y-----WCGIEKTGNDLGVTVQVTDPAVPTQETSSSPTLT 142
 DB 113 YNFRFISDSNRWLDVK-----GTVIVTTDPS-----PTIT 145
 RESULT 9
 LIB2 HUMAN STANDARD; PRT; 598 AA.
 ID LIB2 HUMAN STANDARD; Q8NHJ7; Q8NHJ8;
 AC Q8N423; O75017; Q8NHJ7; Q8NHJ8;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor subfamily B member 2 precursor
 DE (leukocyte immunoglobulin-like receptor 2) (LIR-2) (Immunoglobulin-
 DE like transcript 4) (ILT-4) (Monocyte/macrophage immunoglobulin-like
 DE receptor 10) (MIR-10) (CD85d antigen).
 GN LILRB2 OR LIR2 OR ILT4 OR MIR10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND FUNCTION.
 RC TISSUE=Dendritic cell, and peripheral blood monocytes;
 RX MEDLINE=98208234; PubMed=9548455;
 RT Borges L., Hsu M.-L., Fanger N., Rubin M., Cosman D.;
 RT "A family of human lymphoid and myeloid Ig-like receptors, some of
 RT which bind to MHC class I molecules.";
 RL J. Immunol. 159:5192-5196(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-161; HIS-300
 RP AND CYS-306.
 RA Canavez F.C.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Peripheral blood leukocytes;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sodergren A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP INTERACTION WITH PTPN6 AND FCGR1A, PHOSPHORYLATION, TISSUE
RP SPECIFICITY, AND FUNCTION.
RX MEDLINE=95057019; PubMed=9842885;
RA Fanger N.A., Cosman D., Peterson L., Braddy S.C., Maliszewski C.R.,
RA Borges L.;
RT "The MHC class I binding proteins LIR-1 and LIR-2 inhibit Fc
RT receptor-mediated signaling in monocytes.";
RL Eur. J. Immunol. 28:3423-3434(1998).
[5]
RP FUNCTION.
RX MEDLINE=21864601; PubMed=11875462;
RA Chang C.C., Ciubotariu R., Manavalan J.S., Yuan J., Colovai A.I.,
RA Piazza F., Lederman S., Colonna M., Cortesini R., Dalla-Favera R.,
RA Scudic-Foca N.;
RT "Tolerization of dendritic cells by T(S) cells: the crucial role of
RT inhibitory receptors ILT3 and ILT4.";
RL Nat. Immunol. 3:237-243(2002).
[6]
RP INTERACTION TYPE I MHC ALLELES, AND FUNCTION.
RX MEDLINE=22759998; PubMed=12853576;
RA Shiroishi M., Tsunoto K., Amato K., Shirakihara Y., Colonna M.,
RA Braud V.M., Allan D.S.J., Makadzange A., Rowland-Jones S.,
RA Willcox B.E., Jones E.Y., van der Merwe P.A., Kumagai I., Maenaka K.;
RT "Human inhibitory receptors Ig-like transcript 2 (ILT2) and ILT4
RT compete with CD8 for MHC class I binding and bind preferentially to
RT HLA-G.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8856-8861(2003).
[7]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 22-219.
PubMed=12390682;
RA Willcox B.E., Thomas L.M., Chapman T.L., Heikema A.P., West A.P. Jr.,
RA Bjorkman P.J.;
RT "Crystal structure of LIR-2 (ILT4) at 1.8 Å: differences from LIR-1
RT (ILT2) in regions implicated in the binding of the human
RL cytomegalovirus class I MHC homolog UL18.";
RL BMC Struct. Biol. 2:6-6(2002).
CC -!- FUNCTION: Receptor for class I MHC antigens. Recognizes a broad
CC spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Involved in the
CC down-regulation of the immune response and the development of
CC tolerance. Competes with CD8A for binding to class I MHC antigens.
CC Inhibits FCGR1A-mediated phosphorylation of cellular proteins and
CC mobilization of intracellular calcium ions.
CC -!- SUBUNIT: Binds PTPN6 when phosphorylated. Binds FCGR1A.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8N423-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8N423-2; Sequence=VSP 008458;
CC Note=Alternative use of an acceptor site. No experimental
CC confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed on monocytes and B-cells, and at
CC lower levels on dendritic cells. Detected at low levels in natural
CC killer (NK) cells.
CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.

CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- PTM: Phosphorylated on tyrosine residues. Dephosphorylated by
CC PTPN6.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
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CC
CC EMBL; AF025528; AAB87662.1; -;
CC EMBL; AF283986; AAL36990.1; -;
CC EMBL; AF283987; AAL36991.1; -;
CC EMBL; BC036827; AAL36827.1; -;
CC HSSP; P43626; INKE;
CC Genew; HGNC:6606; LILRB2.
CC MIM; 604815; -;
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00409; Ig; 3.
CC SMART; SM00408; IGC2; 3.
CC PROSITE; P550835; IG_LIKE; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immune response;
KW Immunoglobulin domain; Phosphorylation; Glycoprotein; Antigen;
KW Multigene family; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 598
FT DOMAIN 22 461
FT TRANSMEM 462 482
FT DOMAIN 483 598
FT DOMAIN 27 110
FT DOMAIN 111 229
FT DOMAIN 230 318
FT DOMAIN 330 419
FT SITE 531 536
FT SITE 560 565
FT SITE 590 595
FT DISULFID 49 98
FT DISULFID 144 196
FT DISULFID 156 186
FT DISULFID 245 296
FT DISULFID 345 396
FT CARBOHYD 280 280
FT CARBOHYD 301 301
FT CARBOHYD 340 340
FT VARSPLIC 437 437
FT VARIANT 20 20
FT VARIANT 161 161
FT VARIANT 300 300
FT VARIANT 306 306
FT CONFLICT 322 322
FT CONFLICT 583 583
SQ SEQUENCE 598 AA; 65114 MW; B08463396E45904E CRC64;
Query Match 6.5%; Score 97; DB 1; Length 598;
Best Local Similarity 20.8%; Pred. No. 0.61;
Matches 65; Conservative 40; Mismatches 112; Indels 96; Gaps 13;
QY 24 GPTVNGLRGSLTVQCVSRGWTYLVKWCRCGAIWRDCKILVKTSGSEQVYKRDVSIK 83
DB 332 GPTVNSG---ENVTLIC-----QSWRFHTLLTKAGAADAPLRIRSH 372

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QY 84 DNQKRTFTVTMEDLMKTDADTYWC-----GIEKTGNDLGTVQVTTI 125
DB 373 EYFKYQA-EFPMSPVTSAHAGTYRCYGLNSDPYLLSHPSPELVVSGPSMGSS----- 426
QY 126 DPAPVQTEETSSP-----TUTGHLDN---RHKLKLSVLLPLFTYXLLLVAAALLA 177
DB 427 -PPPTGPISTPAGPDPQLTGTGSDPQSGRLGHVGWIGILVAVVLLLLLLFLFLRLH 485
QY 178 WRMMK-----YQCKAAGMSPEQVLQPLE-----GDLGVADLTQLAGTSRKAT 221
DB 486 RQGHKHTSTQKADFQHPAGAVGPEPTDRGLQWRSSPADAQENLYAAVKOTPE----- 542
QY 222 TKLSSAQVDQVEVYVYTWASLPKEDISYA-----SUTLGAEDQEPYCNXGLSSKLPGR-- 276
DB 543 -----DGVEMDTRAAASAPQDVTYALHSLTLRRKATEP-----PSQER 583
QY 277 -GPBPTEYSIIS 288
DB 584 EPPAEPSIYATLA 596

RESULT 10
PIGR PIG
ID PIGR PIG STANDARD; PRT; 102 AA.
AC Q29244;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE PolymERIC-immunoglobulin receptor (Poly-Ig receptor) (PIGR)
DE (Fragment).
GN PIGR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RL library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -!- FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE
CC BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN
CC TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Also secreted.
CC -----
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CC -----
CC EMBL; F14851; CAA23294.1; -
CC InterPro; IPR007110; IG-LIKE.
CC PROSITE; PS50835; IG_LIKE; PARTIAL.
KW Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein.
FT NON TER 1
FT NON TER 102
SQ SEQUENCE 102 AA; 11205 MW; 82C915264B1508B8 CRC64;

Query Match
Best Local Similarity 6.4%; Score 95.5; DB 1; Length 102;
Matches 24; Conservative 16; Mismatches 49; Indels 1; Gaps 1;

QY 25 PTVNGLRGSITVQCYSRSGWETYLKWCRAIWRDKILVTSQSEQVKKRDRVSIKD 84
DB 9 PELIYGLRGSVTFDCALGQEMANVAKELCQLKNGKTCNVVINTLKKKAQDFEGRILLTP 68
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QY 85 NQKRTFTVTMEDLMKTDADTYWCIEKGTG 114
DB 69 -KENGHSFVHTGLRKEDAGHYLCGXHPDG 97

RESULT 11
SHS1_BOVIN
ID SHS1_BOVIN STANDARD; PRT; 506 AA.
AC O46631; O46632;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-cytosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPs-1) (inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (Sirp-alpha-1) (Myd-1 antigen).
GN PTPNS1 OR SHPS1 OR SIRP OR MYD1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.; AND VARIANTS SER-23; ALA-28; LEU-61; ARG-70;
RP HIS-120; 125-GLN; 129-GLY; 129-HIS; 132-VAL; ASN-145; VAL-153;
RP ASP-203; ARG-261; LEU-302; LEU-316; ARG-337; ASN-367; LEU-422; PHE-429
RP AND GLU-433.
RC STRAIN=Frison; TISSUE=Peripheral blood;
RX MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells.";
RT Eur. J. Immunol. 28:1-11(1998).
RL -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6,
CC PTPN11 and other binding partners from the cytosol to the
CC plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC outgrowth and glial cell attachment. May play a key role in
CC intracellular signaling during synaptogenesis and in synaptic
CC function. Involved in the negative regulation of
CC receptor tyrosine kinase-coupled cellular responses induced by
CC cell adhesion, growth factors or insulin. Mediates negative
CC regulation of phagocytosis, mast cell activation and dendritic
CC cell activation. CD47 binding prevents maturation of immature
CC dendritic cells and inhibits cytokine production by mature
CC dendritic cells (By similarity).
CC -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC Binds JAK2 irrespective of its phosphorylation status and forms a
CC stable complex. Binds SCAP1 and/or SCA2. The resulting complex
CC recruits FVB. Binds FGR and PTK2B (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen macrophages.
CC Detected in skin dendritic cells.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y11045; CAA71942.1; -
CC EMBL; Y11046; CAA71943.1; -
CC InterPro; IPR007110; IG-LIKE.
CC InterPro; IPR003597; IG_C1.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; IG; 3.
```


KW Repeat; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 823
 FT DOMAIN 24 379
 FT TRANSMEM 380 400
 FT DOMAIN 401 823
 FT DOMAIN 42 128
 FT DOMAIN 156 249
 FT DOMAIN 258 360
 FT DOMAIN 135 145
 FT DOMAIN 483 772
 FT NP BIND 489 497
 FT BINDING 519 519
 FT ACT SITE 628 628
 FT MOD_RES 659 659
 FT DISULFID 65 110
 FT DISULFID 181 233
 FT DISULFID 280 344
 FT CARBOHYD 86 86
 FT CARBOHYD 126 126
 FT CARBOHYD 148 148
 FT CARBOHYD 230 230
 FT CARBOHYD 243 243
 FT CARBOHYD 267 267
 FT CARBOHYD 299 299
 FT CARBOHYD 320 320
 FT CARBOHYD 333 333
 SQ SEQUENCE 823 AA; 92299 MW; 42BF3CC4EA02FD43 CRC64;
 Query Match 6.2%; Score 92.5; DB 1; Length 823;
 Best Local Similarity 21.6%; Pred. No. 2.4;
 Matches 58; Conservative 41; Mismatches 86; Indels 83; Gaps 13;
 QY 25 PTTVNGRLSGTLTQVYRSGWETYLKWCRCGAIWRDCKLVKTSGE-----QEV 75
 DB 265 PANASAVVGDDVEFCVKYVSDAQPHIQWIKH-----VERNGSKYGDGLPYLQVL 314
 QY 76 KDRVSIKDNQ-----KRFRTVTMEDLMKTDADTYWCGIEKTCNDLGV---TVQVITD 126
 DB 315 KAAGVNTTDKIEVLYIRNVTF-----EDAGEYTC---LAGNSIGISFHTAWLTVL 362
 QY 127 PAPVTOETSSPTLTGHLDNRHKLKLVLLPLIFTXLLLVAAASLLAWRMKYYQK 186
 DB 363 PAPEKEKEFTSP-----DYLEIAIYCYGVFLACWL---TVLCRMKNTTK 408
 QY 187 AAGMSPEQVQLPGLGDL-----CYADLTQLAGTSPR-KATKLGSS-----A 227
 DB 409 -----PDPSSQPAVHKLTTRPLRRQVTVSADSSSMNSNTPLVRLITRLSSTADAPMLA 463
 QY 228 QVDQVEVEYVTVMASLPKEDISVASITLG 255
 DB 464 GVSEYE-----LPDPKWEFFRDKLTJG 486
 RESULT 13
 ID TVAI RABIT STANDARD; PRT; 134 AA.
 AC P06322;
 DT 01-JAN-1988 (Rel. 05, Created)
 DT 01-JAN-1988 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE T-cell receptor alpha chain V region RL-5 precursor.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86177569; PubMed=3485798;
 RA Marche P.N., Kindt T.J.;
 RT "Two distinct T-cell receptor alpha-chain transcripts in a rabbit
 T-cell line: implications for allelic exclusion in T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2190-2194 (1986).

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC EMBL; M12885; AAA31469.1; --
 DR PIR; A02013; RWRBAV.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003599; IG.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW T-cell; Receptor; Immunoglobulin domain; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134
 FT DOMAIN 21 114
 FT DOMAIN 115 134
 FT CARBOHYD 134 134
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14856 MW; A29F3F8570BEE15E CRC64;
 Query Match 6.1%; Score 92; DB 1; Length 134;
 Best Local Similarity 20.9%; Pred. No. 0.24;
 Matches 28; Conservative 39; Mismatches 55; Indels 12; Gaps 5;
 QY 4 LFLYLLFLW---SGYSIATQITGPTVNGRLSGTLTQVYRSGWETYLKWCRCGAIWR 60
 DB 8 VTVVLLITVTRTNGASV-TQTEGPVILS--EGSSLTLCNYSQTSYGFLEFYVQ-YLHE 63
 QY 61 DCKILVKTSGSQEQVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTCNDLQVT 120
 DB 64 GPQLLOSTENQORVHEQGHFATFKDSSPHLHKSSQLQSDSAVYVCALAR-----GAS 118
 QY 121 VQVITDPAFVQEE 134
 DB 119 NKLTLGTGTLKVE 132
 RESULT 14
 ID HCDR_XAMP2 STANDARD; PRT; 249 AA.
 AC Q56840;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 2-(R)-hydroxypropyl-CoM dehydrogenase (EC 1.1.1.268).
 OS Xanthobacter sp. (strain Py2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Xanthobacter.
 OC NCBI_TaxID=78245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95219103; PubMed=7704278;
 RA Swaving J., Weijers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;
 RT "Complementation of Xanthobacter Py2 mutants in epoxyalkane
 degradation; expression and nucleotide sequence of the complementing
 DNA fragment.";
 RL Microbiology 141:477-484 (1995).
 RN [2]
 RP SEQUENCE OF 1-10, AND CHARACTERIZATION.
 RX MEDLINE=98070376; PubMed=9405410;
 RA Allen J.R., Ensign S.A.;
 RT "Purification to homogeneity and reconstitution of the individual
 components of the epoxide carboxylase multi-protein enzyme complex
 from Xanthobacter strain Py2.";
 RL J. Biol. Chem. 272:32121-32128 (1997).
 CC -!- FUNCTION: Catalyzes the oxidation of 2-(R)-hydroxyalkyl thioesters

RA Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee Y.C.,
 RA "Activating signal cointegrator 2 belongs to a novel steady-state
 RT complex that contains a subset of trithorax group proteins.";
 RL Mol. Cell. Biol. 23:140-149(2003).
 CC -!- FUNCTION: Belongs to the ASC-2/NCOA6 complex (ASCOM), a
 CC coactivator complex of nuclear receptors, involved in
 CC transcriptional coactivation. MLL3 may be a catalytic subunit of
 CC this complex, which weakly methylates lys-4 of histone H3. This is
 CC a specific tag for epigenetic transcriptional activation. May be
 CC involved in leukemogenesis and developmental disorder.
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine =
 CC S-adenosyl-L-homocysteine + histone N(6)-methyl-L-lysine.
 CC -!- SUBUNIT: Belongs to the ASC-2/NCOA6 complex (ASCOM), which
 CC contains ASC-2/NCOA6, the retinoblastoma-binding protein RBQ-3/
 CC RBBP5, alpha- and beta-tubulins, the trithorax group proteins
 CC MLL2 and MLL3, and ASH2/ASCL2. Interacts with histone H3.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8NEZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8NEZ4-2; Sequence=VSP_008561, VSP_008562;
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and ovary, followed
 CC by brain and liver. Also expressed in placenta, peripheral
 CC blood, fetal thymus, heart, lung and kidney. Within brain,
 CC expression was highest in hippocampus, caudate nucleus, and
 CC substantia nigra. Not detected in skeletal muscle and fetal liver.
 CC -!- DOMAIN: The SET domain interacts with histone H3 but not H2A, H2B
 CC and H4, and may have a H3 lysine specific methylation activity.
 CC -!- MISCELLANEOUS: Found in a critical region of chromosome 7, which
 CC is commonly deleted in malignant myeloid disorders. Partial
 CC duplication of the MLL3 gene are found in the juxtacentromeric
 CC region of chromosomes 1, 2, 13 and 21. Juxtacentromeric
 CC reshuffling of the MLL3 gene has generated the BAGE genes.
 CC -!- SIMILARITY: Belongs to the TRX/MLL family.
 CC -!- SIMILARITY: Contains 1 DHHC-type zinc finger.
 CC -!- SIMILARITY: Contains 6 PHD-type zinc fingers.
 CC -!- SIMILARITY: Contains 1 post-SET domain.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- SIMILARITY: Contains 1 SET domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AY024361; AAK00583.1; -;
 DR EMBL; AF264750; AAF74766.2; -;
 DR EMBL; AC006017; AAD45822.1; -;
 DR EMBL; AC104632; -; NOT ANNOTATED CDS.
 DR EMBL; AC005631; -; NOT ANNOTATED_CDS.
 DR EMBL; AB040939; BAA96030.2; -;
 DR EMBL; AK022687; BAB14179.1; -;
 DR EMBL; AK075113; BAC11409.1; -;
 DR EMBL; AL833924; CAD38780.1; -;
 DR Genew; HGNC:13726; MLL3.
 DR MIM; 606833; -;
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR003889; FYRICH_C.
 DR InterPro; IPR003888; FYRICH_N.
 DR InterPro; IPR000910; HMG_12_box.
 DR InterPro; IPR003616; PostSET.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR001594; Znf_DHHC.
 DR InterPro; IPR001965; Znf_PHD.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00505; HMG_box; 1.
 DR Pfam; PF00628; PHD; 6.

DR Pfam; PF00856; SET; 1.
 DR SMART; SM00542; FYRC; 1.
 DR SMART; SM00541; FYRN; 1.
 DR SMART; SM00398; HMG; 1.
 DR SMART; SM00249; PHD; 8.
 DR SMART; SM00508; PostSET; 1.
 DR SMART; SM00317; SET; 1.
 DR PROSITE; PS00354; HMG1_Y; 1.
 DR PROSITE; PS00868; POST_SET; 1.
 DR PROSITE; PS0280; SET; 1.
 DR PROSITE; PS0216; ZF_DHHC; 1.
 DR PROSITE; PS01359; ZF_PHD_1; 5.
 DR PROSITE; PS0016; ZF_PHD_2; 6.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 KW Transferase; Methyltransferase; Chromatin regulator; Activator;
 KW DNA-binding; Nuclear protein; Transcription regulation; Coiled coil;
 KW Zinc-finger; Repeat; Alternative splicing; Polymorphism.
 FT ZN_FING 341 391 PHD-TYPE 1.
 FT ZN_FING 344 389 RING-TYPE.
 FT ZN_FING 348 438 PHD-TYPE 2.
 FT ZN_FING 436 489 DHHC-TYPE.
 FT ZN_FING 464 520 PHD-TYPE 3.
 FT ZN_FING 957 1010 PHD-TYPE 4.
 FT ZN_FING 1007 1057 PHD-TYPE 5.
 FT ZN_FING 1084 1139 PHD-TYPE 6.
 FT DOMAIN 4770 4891 SET.
 FT DOMAIN 4895 4911 POST-SET.
 FT DOMAIN 92 112 COILED COIL (POTENTIAL).
 FT DOMAIN 644 672 COILED COIL (POTENTIAL).
 FT DOMAIN 1338 1366 COILED COIL (POTENTIAL).
 FT DOMAIN 1754 1787 COILED COIL (POTENTIAL).
 FT DOMAIN 3054 3081 COILED COIL (POTENTIAL).
 FT DOMAIN 3173 3272 COILED COIL (POTENTIAL).
 FT DOMAIN 3391 3433 COILED COIL (POTENTIAL).
 FT DNA_BIND 34 46 A.T HOOK (BY SIMILARITY).
 FT DOMAIN 1719 1796 GLN-RICH.
 FT DOMAIN 1834 2281 PRO-RICH.
 FT DOMAIN 2412 2630 PRO-RICH.
 FT DOMAIN 2690 2786 ASP-RICH.
 Query Match 6.1%; Score 92; DB 1; Length 4911;
 Best Local Similarity 25.3%; Pred. No. 27;
 Matches 59; Conservative 32; Mismatches 84; Indels 58; Gaps 13;
 QY 86 QKQRTFTVMDLMKTDADTWCG-----IEKTNDLGVTVQVTI-----DPAP 129
 Db 616 EKQISNEVDSLDKMSSEVGHICGEDQIEDKVEVTEVTVTHQITVQEQQLLEPEP 675
 QY 130 VTQETSSSPTLTGHLDNRKLLKLSVLLPLFTI-----XLLLLVAASLLAWRM-KY 183
 Db 676 VVRESRPP-----KLWVESVTLPLETLVSPHEESISLCPEQLVIERLQGEK 724
 QY 184 QOK-----AAGMSPQVLPLEGLDLCYADLTQLAGTSPRKATTKLSSAQVDQVEVVT 238
 Db 725 EQKENSELSTGLMDSEMTPTIEG--CVKDVSVQ-GGKS-----IKLSS-----ETESSFS 772
 QY 239 MASLPKEDISYA---SLTLGAEDQETPCYCNWGLSSXLPGRGPPEPTREYSTIS 288
 Db 773 SADISKADVSSSPTPSDLPSHMLHNT--PSALSS-----SAGNIMPTTIVISVT 820
 Search completed: September 16, 2004, 12:37:46
 Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:35:20 ; Search time 32 Seconds
(without alignments)
467.860 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 1499

Sequence: 1 MPELLYLLFLWLSGYSIAT.....SXLPGRGPEPTETISRP 290

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCRUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	451.5	30.1	201	3	US-08-955-937A-2
2	451.5	30.1	201	3	US-09-300-985-2
3	434	29.0	195	3	US-08-955-937A-4
4	434	29.0	195	3	US-09-300-985-4
5	329.5	22.0	298	4	US-09-582-934-2
6	323	21.5	301	4	US-09-582-934-1
7	197.5	13.2	164	4	US-09-582-934-3
8	197.5	10.6	624	2	US-08-642-406A-22
9	159.5	10.6	624	4	US-09-199-534-22
10	159.5	10.6	624	4	US-09-199-534-22
11	159.5	10.6	773	3	US-08-434-000A-2
12	159.5	10.6	773	4	US-09-312-157-2
13	153	10.2	771	3	US-08-434-000A-8
14	153	10.2	771	4	US-09-312-157-8
15	145.5	9.7	769	3	US-08-434-000A-10
16	145.5	9.7	769	4	US-09-312-157-10
17	134.5	9.0	608	4	US-09-095-385-4
18	133.5	8.9	746	3	US-08-434-000A-4
19	133.5	8.9	746	4	US-09-312-157-4
20	132.5	8.8	757	3	US-08-434-000A-6
21	132.5	8.8	757	4	US-09-312-157-6
22	127.5	8.5	294	6	S260223-1
23	125	8.3	303	4	US-08-985-950-2
24	125	8.3	303	4	US-09-546-049-2
25	121.5	8.1	334	4	US-09-197-970B-7
26	113.5	7.6	230	4	US-09-148-545-214
27	113.5	7.6	231	4	US-09-148-545-215

28 111 7.4 109 3 US-08-961-564A-9
29 107 7.1 46 3 US-08-955-937A-12
30 107 7.1 46 3 US-09-300-985-12
31 105 7.0 451 1 US-08-287-001A-2
32 105 7.0 451 5 PCT-US95-09941-2
33 100 6.7 307 4 US-09-197-970B-3
34 99 6.6 128 4 US-09-450-520A-6
35 97 6.5 598 4 US-09-310-463-10
36 97 6.5 598 4 US-08-842-448A-10
37 97 6.5 615 3 US-08-985-950-16
38 97 6.5 615 3 US-08-985-950-18
39 97 6.5 615 4 US-09-546-049-16
40 97 6.5 615 4 US-09-546-049-18
41 95.5 6.4 255 2 US-07-690-192-4
42 94 6.3 128 2 US-08-470-139-26
43 94 6.3 128 4 US-09-347-061-26
44 93.5 6.2 165 4 US-09-148-545-149
45 93 6.2 241 2 US-07-916-098A-56

ALIGNMENTS

RESULT 1
US-08-955-937A-2
; Sequence 2, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUIJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALENGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAINER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-955-937A-2

Query Match 30.1%; Score 451.5; DB 3; Length 201;
Best Local Similarity 49.8%; Pred. No. 1.1e-38;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;

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QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLGS---CFSIQGPESVRAPEQGSLLTVQCHYKQGWETIYIKWCGVGRWDTCKILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSEQGEKSDRVSIKDNQKRTFTVTMEGLRRDADVYWGIERGPDGLGTQVKVIVDP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTQETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTXLLLLVAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 EGAA-STTASPTNSNMAVFIGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-----QPLEGD 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      173 KGSQVPEEPGEQPIYMFSEPLTKDM 199
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RESULT 2

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US-09-300-985-2
; Sequence 2, Application US/09300985A
; Patent No. 6232441

```

GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; FILE OF INVENTION: SUPERFAMILY
; CURRENT APPLICATION NUMBER: US/09/300,985A

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; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 201
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

```

```

US-09-300-985-2

```

```

Query Match      30.1%; Score 451.5; DB 3; Length 201;
Best Local Similarity 49.8%; Pred. No. 1.1e-38;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;

```

```

QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLGS---CFSIQGPESVRAPEQGSLLTVQCHYKQGWETIYIKWCGVGRWDTCKILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSEQGEKSDRVSIKDNQKRTFTVTMEGLRRDADVYWGIERGPDGLGTQVKVIVDP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTQETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTXLLLLVAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 EGAA-STTASPTNSNMAVFIGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-----QPLEGD 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      173 KGSQVPEEPGEQPIYMFSEPLTKDM 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 3

```

US-08-955-937A-4
; Sequence 4, Application US/08955937A
; Patent No. 6020161

```

GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED

```

```

; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997

```

```

; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

```

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 195 amino acids

```

```

; TYPE: amino acid

```

```

; STRANDEDNESS: single

```

```

; TOPOLOGY: linear

```

```

; MOLECULE TYPE: protein

```

```

;
US-08-955-937A-4

```

```

Query Match      29.0%; Score 434; DB 3; Length 195;
Best Local Similarity 49.5%; Pred. No. 6.5e-37;
Matches 100; Conservative 21; Mismatches 57; Indels 24; Gaps 8;

```

```

QY      8 LLLFWLSGYSIATQITGTTVNGLERGSLTVQCYVRSWETYLKWCRCGAIWRDCKILVK 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7 LLLLSLGS---CFSIQGPESVRAPEQGSLLTVQCHYKQGWETIYIKWCGVGRWDTCKILIE 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      68 TSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTVQVITDP 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      64 TRGSEQGEKSDRVSIKDNQKRTFTVTMEGLRRDADVYWGIERGPDGLGTQVKIDXP 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      128 APVTQETSSSPT-----LTGHHLDNRHKLKLSVLLPLFTXLLLLVAASLLAWRM 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      124 RGSQGPQQSSPTNSNMAVFIGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 173
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      182 KYQQAAGMSPEQVL-QPLEGD 202
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      174 KGSQV-----PEEPXEQPIYND 191
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 4

```

US-09-300-985-4
; Sequence 4, Application US/09300985A
; Patent No. 6232441

```

GENERAL INFORMATION:

```

; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A

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; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (122) (170) (184)
US-09-300-985-4

Query Match      29.0%; Score 434; DB 3; Length 195;
Best Local Similarity 49.5%; Pred. No. 6.5e-37;
Matches 100; Conservative 21; Mismatches 57; Indels 24; Gaps 8;

Qy 8 LLLFWLSGYSIATQITGPTTWNGLRGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVK 67
Db 7 LLLLSLGG---CPSIQGESVRAPEQGSLLTVQCHYKQGWETYLKWCRCGVRWMDTCKILIE 63

Qy 68 TSGSEQEVKDRVSIKDNOKNRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTQVITDP 127
Db 64 TRGSEQEKSDRVSIKDNOKRFTFTVTMEGLRDDADVWCGIERGPDGLGTQVKIDCXP 123

Qy 128 APVTQETSSTSP-----LTGHHLDNRHKLKLSVLLPLIFITXLLLVAASLLAWRMW 181
Db 124 RGSFPQQSQSPINSNMAVIGSHKRN-HYMLLVFKVPI-----LLILWAXL--W--L 173

Qy 182 KYQKAGMSPQVL-OPLEGD 202
Db 174 KGSQRV-----PEEPXEQPIYMD 191
```

```

RESULT 5
US-09-582-934-2
; Sequence 2, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-2

Query Match      22.0%; Score 329.5; DB 4; Length 298;
Best Local Similarity 32.9%; Pred. No. 8.1e-26;
Matches 105; Conservative 51; Mismatches 98; Indels 65; Gaps 15;

Qy 8 LLLFWLSG---YSIATQITGPTTWNGLRGSLTVQCVYRSGWETYLKWCRCGAIWRDCKI 64
Db 7 LLLIWPQCFALSKCRTVAGPW-----GSLSVQCPYEKEHRTLNKYWCRPPQIFLDCX 59

Qy 65 LVKTSQSEVQRDRVSIKDNOKNRTFTVTMEDLMKTDADTYWCGIE---KTGNDLGVT 120
Db 60 IVETKGSAGK-RNGRVSIKDSFANLSFTVLTLENLTEDAGTYWCGVDTPLWRDPHPVVE 118

Qy 121 VQVTI-----DPAPVTQETS-----SSPTL-----TGHHLDNRHKL-----LKL 155
Db 119 VEVSVFPASTSMTPASITAAKTSTITTAFFPVSSSTTLFAVGATHSASIQEETEEVNVSQL 178

Qy 156 SVLLPLIFITXLLLVAASLLAWRMWYQKQ--AAG-----MSPEQVLQPLEGDLGYAD 207
Db 179 PLLLSLL-ALLLLLVGASLLAWRFQKWKIKAGDHSELSQNPQA--ATQSELHYANL 235

Qy 208 LTIQLAGTSPRKATTKLSAQVDQVEYVTVWASIPKSDISYASLTGAEODEPTVCNMG 267
Db 236 LELLMWPLQEKAPPR-----EVEVEYSTVAS--PREELHYASVVFDS-----NTN 279

Qy 268 XLSSXLPGRGPEEPTYSTISR 289
Db 280 RTAAQRP-REEBPDSYDVIRK 300
```

RESULT 7

US-09-582-934-3
; Sequence 3, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-3

Query Match 13.2%; Score 197.5; DB 4; Length 164;
Best Local Similarity 36.9%; Pred. No. 1.5e-12;
Matches 48; Conservative 23; Mismatches 40; Indels 19; Gaps 4;
QY 22 ITGPTTVNGLRSLTVQCVYRSGWETVYKWCRCGAIWRDCKILVKTSGSEQEYKRDVRS 81
DB 11 VAGPW-----GSLSVQCPYEKEHRTLNKYWCRRPPQIFLCKIVETKGSAGK-RNGRVS 62
QY 82 IKDNQKRTFTVTMEDLMKTDADTYWQIE-----KTGNDLGVTVQVTI-----DPAPV 130
DB 63 IRDSPANLSFTVLENTTEEDAGTYWCGVDPFWLRDFHPVVEVSVFPASTSMTPASI 122
QY 131 TQETSSSPT 140
DB 123 TAAKTSITT 132

RESULT 8
US-08-642-406A-22
; Sequence 22, Application US/08642406A
; Patent No. 5959177
; GENERAL INFORMATION:
; APPLICANT: Heint, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; TITLE OF INVENTION: SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5959177th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,406A
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/591,823
; FILING DATE: 02-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/427,765

FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 184.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-406A-22
Query Match 10.6%; Score 159.5; DB 2; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;
QY 4 LTYLTLFWLSCYSTAT-----QITGPTTVNGLRSLTVQCVYRSGWET--YIKW 52
DB 1 MALFLITCLAVPSAATAQSSLLGPSIFGPEVNVLESDSVITCYPTTSVTRHSRKF 60
QY 53 WCRGAIWRDCKILVKTSGSEQEYKRDVRSIKDNQKRTFTVTMEDLMKTDADTYWQIEK 112
DB 61 WCRBESRCVTLASTGVTSGEYS-GRGKLTDFDPKGEFVTVDTQNDGSGYKCGV 119
QY 113 TGN--DLGVTVQVTIDPAP---VTQETSSSPTLTGHHLDNRHKLKLSVLLPFI 165
DB 120 NGRGLDFGVNLVSKPEPDDVYKQYESYTVITCPFTYATRLKK-----SFYKVED 173
QY 166 -XLLLVLAASLLAWRMKYQKCAKMSPEQVLPGLGCLCYADLTQLAGTSPRKATKL 224
DB 174 GELVLIIDSSSKKADPKYKGR-----ITLQQTSTAKEFTVTI 212
QY 225 SSAQVDQVEYVYVMA---SLPKEDISYASLTGAEQDEPTYNMG 267
DB 213 KHLQNDAG-QYVCSGSDPTAEQNVDLRLTLC-----LYGNLG 253

RESULT 9
US-09-199-534-22
; Sequence 22, Application US/09199534
; Patent No. 6329569
; GENERAL INFORMATION:
; APPLICANT: Heint, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; TITLE OF INVENTION: SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 6329569th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,534
; FILING DATE: 25-NOV-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,406
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/427,765

FILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 184.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-199-534-22

Query Match 10.6%; Score 159.5; DB 4; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLSGYSIAT-----QITGPTTVNGLERGLTVQCVYRSGWET--YLKW 52
Db 1 MALFLLTCLLAVPSAATAQSSLLGPSSIFGPGEVNVLGDSVSITCYPTTTSVTRHSRKF 60

QY 53 WCRGAIWRDCKILVKTSQSEVKEVDKYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEK 112
Db 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPDKGEFVTVTDLTQNDSGSYKCGVGV 119

QY 113 TGN--DLGVTVQVTTIDPAP---VTQETSSSPILTGHLDNRHKLKLSVLLPLIFTI-- 165
Db 120 NGRGLDFGVNVLVSQKPEPDVVYKQYESYVITTCPTVATRLQKK-----SFYKVED 173

QY 166 -XLLLVAAASLLAMRMKYQKQKAGMSPEQVLPQLEGDLCLYADLTQLAGTSRKAATKL 224
Db 174 GELVLIIDSSSKAKDPYKGR-----ITLQIQSTTAKEFTVTI 212

QY 225 SSAQVDQVEVEYVWMA---SLPKEDISYASILTGAEDQPTCYNMG 267
Db 213 KHLQNDAG-QYVCQSGSDPTAEQVNDLRLTLPGL-----LYGNLG 253

RESULT 10
US-09-199-534-22
Sequence 22, Application US/09199534
Patent No. 6417429
GENERAL INFORMATION:
APPLICANT: Hein, Mich B.
Ma, Julian K.C.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
SECRETORY ANTIBODIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. 6417429th Torrey Pines Road, TPC-8
City: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199/534
FILING DATE: 25-No. 6417429-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,406
FILING DATE: <unknown>
APPLICATION NUMBER: US 07/427,765

FILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 184.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-199-534-22

Query Match 10.6%; Score 159.5; DB 4; Length 624;
Best Local Similarity 24.0%; Pred. No. 9.6e-08;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLSGYSIAT-----QITGPTTVNGLERGLTVQCVYRSGWET--YLKW 52
Db 1 MALFLLTCLLAVPSAATAQSSLLGPSSIFGPGEVNVLGDSVSITCYPTTTSVTRHSRKF 60

QY 53 WCRGAIWRDCKILVKTSQSEVKEVDKYSIKDNQKRTFTVTMEDLMKTDADTYWCGIEK 112
Db 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPDKGEFVTVTDLTQNDSGSYKCGVGV 119

QY 113 TGN--DLGVTVQVTTIDPAP---VTQETSSSPILTGHLDNRHKLKLSVLLPLIFTI-- 165
Db 120 NGRGLDFGVNVLVSQKPEPDVVYKQYESYVITTCPTVATRLQKK-----SFYKVED 173

QY 166 -XLLLVAAASLLAMRMKYQKQKAGMSPEQVLPQLEGDLCLYADLTQLAGTSRKAATKL 224
Db 174 GELVLIIDSSSKAKDPYKGR-----ITLQIQSTTAKEFTVTI 212

QY 225 SSAQVDQVEVEYVWMA---SLPKEDISYASILTGAEDQPTCYNMG 267
Db 213 KHLQNDAG-QYVCQSGSDPTAEQVNDLRLTLPGL-----LYGNLG 253

RESULT 11
US-08-434-000A-2
Sequence 2, Application US/08434000A
Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 1

```

; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Rabbit polyimmunoglobulin receptor
US-08-434-000A-2

Query Match 10.6%; Score 159.5; DB 3; Length 773;
Best Local Similarity 24.0%; Pred. No. 1.3e-07;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLGSYSIAT-----QITGPTTVNGLERSLTVQCVYRSGMET--YLKW 52
DB 1 MALFLLTCLLAVFSAATAQSSLLGPSSIFGGEVNVLEGSVSITCYPTTSVTRHSRKF 60
QY 53 WCRGAIWRDCKILVKTSGSEGEVKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEK 112
DB 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPKGFEVTVTDLTQNDSSGSKCGVGV 119
QY 113 TGN--DLGVTVQVITIDPAP---VTQETSSSPTLTGHLDNRHKLKLVLLPLIFTI-- 165
DB 120 NGRGLDFGVNVLVSQKPEPDDVVKQYESYVTTTCPTTYATRLQKK-----SFYKVED 173
QY 166 -XLILLVAASLLAWRMKYQOKAAGMSPQVLQPLEGLDCLVADLTQLAGTSPRKATTKL 224
DB 174 GELVLIIDSSSKEAKDPYKGR-----ITLQIQSTTAKEFTVTI 212
QY 225 SSAQVDQVEVEYVTMA-----SLPKEDISYASLTGAEDQEPPTCNMG 267
DB 213 KHLQLNDAG-QYVCQSGSDPTAEQNVDLRLTLTGL-----LYGNLG 253

RESULT 12
US-09-312-157-2
; Sequence 2, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 773 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Rabbit polyimmunoglobulin receptor
US-09-312-157-2

Query Match 10.6%; Score 159.5; DB 4; Length 773;
Best Local Similarity 24.0%; Pred. No. 1.3e-07;
Matches 69; Conservative 49; Mismatches 112; Indels 57; Gaps 11;

QY 4 LTLVLLFWLGSYSIAT-----QITGPTTVNGLERSLTVQCVYRSGMET--YLKW 52
DB 1 MALFLLTCLLAVFSAATAQSSLLGPSSIFGGEVNVLEGSVSITCYPTTSVTRHSRKF 60
QY 53 WCRGAIWRDCKILVKTSGSEGEVKRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEK 112
DB 61 WCREESGRCVTLASTGYTSQEYS-GRGKLTDFPKGFEVTVTDLTQNDSSGSKCGVGV 119
QY 113 TGN--DLGVTVQVITIDPAP---VTQETSSSPTLTGHLDNRHKLKLVLLPLIFTI-- 165
DB 120 NGRGLDFGVNVLVSQKPEPDDVVKQYESYVTTTCPTTYATRLQKK-----SFYKVED 173
QY 166 -XLILLVAASLLAWRMKYQOKAAGMSPQVLQPLEGLDCLVADLTQLAGTSPRKATTKL 224
DB 174 GELVLIIDSSSKEAKDPYKGR-----ITLQIQSTTAKEFTVTI 212
QY 225 SSAQVDQVEVEYVTMA-----SLPKEDISYASLTGAEDQEPPTCNMG 267
DB 213 KHLQLNDAG-QYVCQSGSDPTAEQNVDLRLTLTGL-----LYGNLG 253

RESULT 13
US-08-434-000A-8
; Sequence 8, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A

```

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION: Mouse Polyimmunoglobulin Receptor
; US-08-434-000A-8

Query Match 10.2%; Score 153; DB 3; Length 771;
Best Local Similarity 22.4%; Pred. No. 6.2e-07;
Matches 76; Conservative 46; Mismatches 144; Indels 74; Gaps 12;

QY 3 LLLYLLFWLSGYSIATQITGPTTVNGLSLTQCVYRSGWETYL-----KWCRCGA 57
DB 5 LFTLLVTVF--SGVSTKSPIFGQEVSSIEGDSVITCYYP---DTSVNRHTRKYWCROG 59
QY 58 IWRDCKILVTSGEQVKRDRSVIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTDNDL 117
DB 60 ASGMCTLLISNGVLSKEYSGRANLINFENNIFVINIEQLTQDDTGSYKCGLGTSNRGL 119
QY 118 GVTQVTTIDPAP-----VTQE-----ETSSPTLTGHH 145
DB 120 SFDVLSVQVPELPSDTHVTYKDIGRNVITIECPFKRENVPKSKLCKTNQSCELV--- 176
QY 146 LDRHKLKLSVLLPLIF---TIXLLLVAAASLLAWRMKYQKKAAGMSPE-----Q 194
DB 177 IDSTEKNVPSYIGRAKLPKMGTDLTVFYVNIHSLTHNDAGLYICQAGEGPSADKKNVDLQ 236
QY 195 VLQPLEGLCYADLTQLA-----GTSFRKATTKLSSAQVDQVEVEYVTMAS----- 241
DB 237 VLAP-EPELLYKDLRSSVTPECDLGREVANEAKYLCRMNKETCDVIINTLGKRDPPDEGR 295

RESULT 14
US-09-312-157-8
; Sequence 8, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,157
; FILING DATE: 14-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,000
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-351
; SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION: Mouse Polyimmunoglobulin Receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-312-157-8

Query Match 10.2%; Score 153; DB 4; Length 771;
Best Local Similarity 22.4%; Pred. No. 6.2e-07;
Matches 76; Conservative 46; Mismatches 144; Indels 74; Gaps 12;

QY 3 LLLYLLFWLSGYSIATQITGPTTVNGLSLTQCVYRSGWETYL-----KWCRCGA 57
DB 5 LFTLLVTVF--SGVSTKSPIFGQEVSSIEGDSVITCYYP---DTSVNRHTRKYWCROG 59
QY 58 IWRDCKILVTSGEQVKRDRSVIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTDNDL 117
DB 60 ASGMCTLLISNGVLSKEYSGRANLINFENNIFVINIEQLTQDDTGSYKCGLGTSNRGL 119
QY 118 GVTQVTTIDPAP-----VTQE-----ETSSPTLTGHH 145
DB 120 SFDVLSVQVPELPSDTHVTYKDIGRNVITIECPFKRENVPKSKLCKTNQSCELV--- 176
QY 146 LDRHKLKLSVLLPLIF---TIXLLLVAAASLLAWRMKYQKKAAGMSPE-----Q 194
DB 177 IDSTEKNVPSYIGRAKLPKMGTDLTVFYVNIHSLTHNDAGLYICQAGEGPSADKKNVDLQ 236
QY 195 VLQPLEGLCYADLTQLA-----GTSFRKATTKLSSAQVDQVEVEYVTMAS----- 241
DB 237 VLAP-EPELLYKDLRSSVTPECDLGREVANEAKYLCRMNKETCDVIINTLGKRDPPDEGR 295

RESULT 15
US-08-434-000A-10
; Sequence 10, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:31:24 ; Search time 117 Seconds
(without alignments)
782.054 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 1499
Sequence: 1 MPILLTYLLFWLSGYSIAT.....SXLPGRGPETPEYTSITSRP 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_virus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1493	99.6	290	Q7Z6A6	Q7Z6A6 homo sapien
2	1487	99.2	290	Q8TDQ1	Q8TDQ1 homo sapien
3	1408.5	94.0	293	Q7Z7I5	Q7Z7I5 homo sapien
4	803	53.6	244	Q8NAP5	Q8NAP5 homo sapien
5	727.5	48.5	165	Q7Z7I4	Q7Z7I4 mus sapien
6	725.5	48.4	194	Q8N6D0	Q8N6D0 homo sapien
7	550.5	36.7	283	Q8K4V9	Q8K4V9 mus musculus
8	451.5	30.1	201	Q8IX40	Q8IX40 mus musculus
9	451.5	30.1	238	Q8N6D1	Q8N6D1 homo sapien
10	367	24.5	314	Q7TNS3	Q7TNS3 mus musculus
11	367	24.5	318	Q7TNS6	Q7TNS6 mus musculus
12	364	24.3	318	Q8CFN3	Q8CFN3 mus musculus
13	358.5	23.9	221	Q8VCH2	Q8VCH2 mus musculus
14	351.5	23.4	221	Q8BRU3	Q8BRU3 mus musculus
15	331	22.1	299	Q9UBK4	Q9UBK4 homo sapien
16	330.5	22.0	298	Q9HD97	Q9HD97 homo sapien

ALIGNMENTS

RESULT 1

Q7Z6A6	Q7Z6A6	PRELIMINARY;	PRT;	290 AA.
AC	Q7Z6A6;			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Inhibitory receptor IREM1.			
GN	IREM1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Alvarez-Erico D., Kitzig P., Sayos J., Lopez-Botet M.;			
RT	"Molecular and functional characterization of IREM-1, a novel			
RT	inhibitory receptor expressed by myeloid cells.";			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY303545; AAP57942.1; ..			
KW	Receptor.			
SQ	SEQUENCE 290 AA; 32354 MW; E9D846B417AA99B CRC64;			
Query Match	99.6%;	Score 1493;	DB 4;	Length 290;
Best Local Similarity	99.0%;	Pred. No. 9e-134;		
Matches 287;	Conservative	0; Mismatches	3; Indels	0; Gaps 0;
Qy	1	MPILLTYLLFWLSGYSIATQITGPTTNGLERGSLTVQCVYRSGWYLYKWCRCGAIWR	60	
Db	1	MPILLTYLLFWLSGYSIATQITGPTTNGLERGSLTVQCVYRSGWYLYKWCRCGAIWR	60	
Qy	61	DKKILVKTSQSQEYKVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV	120	
Db	61	DKKILVKTSQSQEYKVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV	120	
Qy	121	VQVTTDPAPVTOETSSSPSTLTGHHLDNRHKLKLSVLLPIFTIXLIIIVAAASLLAWRM	180	
Db	121	VQVTTDPAPVTOETSSSPSTLTGHHLDNRHKLKLSVLLPIFTIXLIIIVAAASLLAWRM	180	

QY 181 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 290
 DB 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 290

RESULT 2
 Q8TDQ1 PRELIMINARY; PRT; 290 AA.
 AC Q8TDQ1;
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE NK inhibitory receptor.
 GN NKIR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li N., Wan T., Zhang W., Cao X.;
 RT "Novel human NK inhibitory receptor NKIR precursor.";
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF251706; AAM19099.1;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001986; EFSF_synth.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00104; EFSF_SYNTHASE_1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Receptor.
 SQ SEQUENCE 290 AA; 32395 MW; D14FC04A047AAD10 CRC64;

Query Match 99.2%; Score 1487; DB 4; Length 290;
 Best Local Similarity 98.6%; Pred. No. 3.4e-133;
 Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPLLTYLLFWLS-GYSIATQITGTTVNGLERGLTVQCYRSGWETYLKWCRCGAIWR 60
 DB 1 MPLLTYLLFWLSGYSIATQITGTTVNGLERGLTVQCYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
 DB 61 DCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120

QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLVAAALLAWR 180
 DB 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLVAAALLAWR 180

QY 181 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 290
 DB 241 SLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 290

RESULT 3
 Q7Z7I5 PRELIMINARY; PRT; 293 AA.
 AC Q7Z7I5;
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Immune receptor expressed on myeloid cells splice variant 1.
 GN IREM1.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
 RT "Molecular and functional characterization of IREM-1, a novel
 RT inhibitory receptor expressed by myeloid cells.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF375480; AAP42152.1;
 KW Receptor.
 SQ SEQUENCE 293 AA; 32655 MW; 66EBEA2F8D3CF43E CRC64;

Query Match 94.0%; Score 1408.5; DB 4; Length 293;
 Best Local Similarity 94.5%; Pred. No. 1e-125;
 Matches 275; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 MPLLTYLLFWLS-GYSIATQITGTTVNGLERGLTVQCYRSGWETYLKWCRCGAIWR 59
 DB 3 LPQLDLMRVISAKSQYSIATQITGTTVNGLERGLTVQCYRSGWETYLKWCRCGAIWR 62

QY 60 RCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
 DB 63 RCKILVKTSGSQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122

QY 120 TVQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLVAAALLAWR 179
 DB 123 TVQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPIFTIXLLLVAAALLAWR 182

QY 180 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTM 239
 DB 183 MKYQQAAGMSPEQVLPLEGDLCLYADLTLOAGTSRKATTKLSSAQVDQVEVEYVTM 242

QY 240 ASLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 290
 DB 243 ASLPKEDISYASLTGAEDQEPYCNMGXLSXLPGRGPEEPTSTSRP 293

RESULT 4
 Q8NAF5 PRELIMINARY; PRT; 244 AA.
 AC Q8NAF5;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hypothetical protein FLJ35438.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RA Ninomiya K., Wagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
 RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK092757; BAC03966.1;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 244 AA; 26643 MW; 2C7C6EAD5F9C7FA5 CRC64;

Query Match 53.6%; Score 803; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 3.8e-68;

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Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 60
Db 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
Db 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
RESULT 5
Q72714 PRELIMINARY; PRT; 165 AA.
AC Q72714;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Immune receptor expressed on myeloid cells splice variant 2.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Erico D., Kitrig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel
RT inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375481; AAP42153.1; -.
KW Receptor.
SQ SEQUENCE 165 AA; 18655 MW; F163D7D366063099 CRC64;
Query Match 48.4%; Score 727.5; DB 4; Length 165;
Best Local Similarity 91.4%; Pred. No. 3.5e-61;
Matches 138; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 3 LPQLDLMRVISAQSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 62
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 63 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122
QY 120 TVQVITDPAVPTQETSSPILTGHHLDNRH 150
Db 123 TVQVITDPAVPTQETSSPILTGHHLDNRH 153
RESULT 6
Q8N6D0 PRELIMINARY; PRT; 194 AA.
AC Q8N6D0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT Tissue-Lung;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028199; AAH28199.1; -.
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 60
Db 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
Db 121 VQVITDPAVPTQETSSPILTGHHLDNR 149
RESULT 7
Q8K4V9 PRELIMINARY; PRT; 283 AA.
AC Q8K4V9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polymeric immunoglobulin receptor 3.
GN PIGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Li N., Chen T., Cao X.;
RT "Novel mouse PIGR3.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251703; AAM19096.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 283 AA; 30777 MW; D6AC98F9C7FD5246 CRC64;
Query Match 36.7%; Score 550.5; DB 11; Length 283;
Best Local Similarity 40.2%; Pred. No. 5.3e-44;
Matches 132; Conservative 31; Mismatches 76; Indels 89; Gaps 6;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 1 MHLSTLVPFLFWITGCTAEDPTGFEVSGEQSGSVTVQCRYSKWDYKRYWCGVPQ 60
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 61 RSKTLVETDASEQLVKNRVSIRDQDFITVTMEDLRMSDAGIYWCITKGLDPMF 120
QY 120 TVQVITDPAVPTQETSSPILTGHHLDNRH 150
Db 121 KVTNIGPAIQVPIITVPTMPITSTTITFTVTTKETSMFEPLTSYSDNHHGSGG 180
QY 151 -----KLLKLSVLLPLFTITXLLVLAASLAWMMKYQCKAAGMSPEQVLPLEGDL 203
Db 181 GEDGVDGDFLDLSVLLPVISAVLLLLVLA----- 210
QY 204 CYADLTQLAGTSPRKATTKLSSAQVDQVEYVTNMLPKEDISYASLTLAGDEQPT 263
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DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 194 AA; 21399 MW; 33B6AABE48F4FD6D CRC64;
Query Match 48.4%; Score 725.5; DB 4; Length 194;
Best Local Similarity 92.6%; Pred. No. 6.8e-61;
Matches 138; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 3 LPQLDLMRVISAQSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 62
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 63 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 122
QY 120 TVQVITDPAVPTQETSSPILTGHHLDN 148
Db 123 TVQVITDPAVPTQETSSPILTGHHLDN 151
RESULT 7
Q8K4V9 PRELIMINARY; PRT; 283 AA.
AC Q8K4V9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polymeric immunoglobulin receptor 3.
GN PIGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Li N., Chen T., Cao X.;
RT "Novel mouse PIGR3.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251703; AAM19096.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 283 AA; 30777 MW; D6AC98F9C7FD5246 CRC64;
Query Match 36.7%; Score 550.5; DB 11; Length 283;
Best Local Similarity 40.2%; Pred. No. 5.3e-44;
Matches 132; Conservative 31; Mismatches 76; Indels 89; Gaps 6;
QY 1 MPILTYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIW 59
Db 1 MHLSTLVPFLFWITGCTAEDPTGFEVSGEQSGSVTVQCRYSKWDYKRYWCGVPQ 60
QY 60 RDCKILVKTSGSEQEVKRDVSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTGNDLGV 119
Db 61 RSKTLVETDASEQLVKNRVSIRDQDFITVTMEDLRMSDAGIYWCITKGLDPMF 120
QY 120 TVQVITDPAVPTQETSSPILTGHHLDNRH 150
Db 121 KVTNIGPAIQVPIITVPTMPITSTTITFTVTTKETSMFEPLTSYSDNHHGSGG 180
QY 151 -----KLLKLSVLLPLFTITXLLVLAASLAWMMKYQCKAAGMSPEQVLPLEGDL 203
Db 181 GEDGVDGDFLDLSVLLPVISAVLLLLVLA----- 210
QY 204 CYADLTQLAGTSPRKATTKLSSAQVDQVEYVTNMLPKEDISYASLTLAGDEQPT 263
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Db 211 -----SSGKHQEEYVYTMAPPFREESVYAAALTLAGLQGEPTY 249
QY 264 CNMGXLSXLPGRG-PERPTREYTSIRP 290
Db 250 GNTGCPITHVPTGLTEETTSYSSIRP 277

RESULT 8
Q8IX40
ID Q8IX40 PRELIMINARY; PRT; 201 AA.
AC Q8IX40;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-OCT-2003 (TREMBLrel. 23, Last sequence update)
DE TREM5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Colonna M.;
RT "Triggering receptor expressed on myeloid cells 5.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF427618; AAN86133.1; -.
DR InterPro; IPR003599; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 201 AA; 22689 MW; 2B8027A488B97CAF CRC64;

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Query Match 30.1%; Score 451.5; DB 4; Length 201;
Best Local Similarity 49.8%; Pred. No. 9e-35; Indels 25; Gaps 8;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;

QY 8 LLLFWLSGYSIATQITGPTVNGLERGLTQCVYRSGWETYLKWCRCGAIWRDCKILVK 67
Db 7 LLLLSLSG---CFSIQGPESVRAPQSGSLTVQCHYKQGWETYLKWCRCGVRWDTCILIE 63
QY 68 TSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTQVTDIP 127
Db 64 TRGSEQSEKSDRVSIKDNQKRTFTVTMEGRDDADVIWCGIERRDPDLGTQVKVIVDP 123
QY 128 APVTQETSSSPT-----LTGHLDNRHKLKLSVLLPFTIXLLLLVAASLLAWRM 181
Db 124 EGAA-STTASPTNSMVAFIGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 172
QY 182 KYQKAAGMSPEQVL-----QPLEGDL 203
Db 173 KGSQVRPEEPGEOPIYMFSEPLTKDM 199

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RESULT 9
Q8NGD1
ID Q8NGD1 PRELIMINARY; PRT; 238 AA.
AC Q8NGD1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor, CMRF35 antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Blood;
RC Tissue-Blood;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028091; AAH28091.1; -.
GO; GO:0004872; F:receptor activity; IEA.

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DR InterPro; IPR003599; IG.
DR SMART; SM007110; IG-like.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27020 MW; 1E7679BE434BB89 CRC64;

Query Match 30.1%; Score 451.5; DB 4; Length 238;
Best Local Similarity 49.8%; Pred. No. 1.1e-34; Indels 25; Gaps 8;
Matches 103; Conservative 22; Mismatches 57; Indels 25; Gaps 8;

QY 8 LLLFWLSGYSIATQITGPTVNGLERGLTQCVYRSGWETYLKWCRCGAIWRDCKILVK 67
Db 44 LLLLSLSG---CFSIQGPESVRAPQSGSLTVQCHYKQGWETYLKWCRCGVRWDTCILIE 100
QY 68 TSGSQEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTDGNDLGVTQVTDIP 127
Db 101 TRGSEQSEKSDRVSIKDNQKRTFTVTMEGRDDADVIWCGIERRDPDLGTQVKVIVDP 160
QY 128 APVTQETSSSPT-----LTGHLDNRHKLKLSVLLPFTIXLLLLVAASLLAWRM 181
Db 161 EGAA-STTASPTNSMVAFIGSHKRN-HYMLLVFKVPI-----LLILVAIL--W--L 209
QY 182 KYQKAAGMSPEQVL-----QPLEGDL 203
Db 210 KGSQVRPEEPGEOPIYMFSEPLTKDM 236

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RESULT 10
Q7TSN3
ID Q7TSN3 PRELIMINARY; PRT; 314 AA.
AC Q7TSN3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MAIR-1a.
GN MAIR-1a.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Totsumoto K., Okoshi Y., Shibuya K., Yamazaki S., Tahara-Hanaoka S.,
RA Honda S., Osawa M., Kuroiwa A., Matsuda Y., Tenen D.G., Iwama A.,
RA Nakauchi H., Shibuya A.;
RT "Paired Activating and Inhibitory Immunoglobulin-like Receptors, MAIR-
RT I and -II, Regulate Mast Cell and Macrophage Activation.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB091765; BAC77074.1; -.
SQ SEQUENCE 314 AA; 35259 MW; DEFF9509C3A1222D CRC64;

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Query Match 24.5%; Score 367; DB 11; Length 314;
Best Local Similarity 34.5%; Pred. No. 1.9e-26;
Matches 108; Conservative 52; Mismatches 113; Indels 40; Gaps 13;

QY 1 MPLLTYLLFWLSGYSIATQITGPTVNGLERGLTQCVYRSGWETYLKWCRCGAIWR 60
Db 10 LPTLLLLFWLPG---CVPJHGPSTMGSGVESLSVSCRVEEFKTKYKWCVRSLKI 66
QY 61 DCKILVKTSQSEVRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIE-----KYG 114
Db 67 LCKDIKVTSSSE-EARSGRVTIRHPDNLFTFTVYESLTLEDADTYMCAVDISLFDGSLG 125
QY 115 NDLGVTQVITI---DPAV--TQETSSPT-----LTGHLDNRHKLKLSVLLP 160
Db 126 FDYFKIELSVVPSDEPGTLETPTVVTSLPTKGPALGNTSGHREHDYVQGLRPLALLS 185
QY 161 LFTIXLLLLVAASLLAWRMKYQKAAGMSPE---QVLPLEGDLCYADLTQLAGTSP 217
Db 186 -VLALLLLFWLVTSLAWRMFQKRLVKADRHFLSQNLQRQASEQNECOY-VNLQLHTWSL 243
QY 218 RKATKLSAQQVDQVEVEVTVMASLPKEDIYSASITLGAEDQEPYCNMGXLSXLPGRG 277

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GN	B230315M08RIK OR MMAC8 OR MAIR-1B.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yoshimoto M., Sekine S., Yazaki M., Sawada M.;
RT	"Molecular cloning of an NK inhibitory receptor-related gene expressed in a mouse microglial cell line, Ra2.";
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Yotsumoto K., Okoshi Y., Shibuya K., Yamazaki S., Tahara-Hanaka S.,
RA	Honda S., Osawa M., Kuroiwa A., Matsuura Y., Tenen D.G., Iwama A.,
RA	Nakauchi H., Shibuya A.;
RT	"Paired Activating and Inhibitory Immunoglobulin-Like Receptors, MAIR-1 and -II, Regulate Mast Cell and Macrophage Activation.";
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB065156; BAC22595.1; -.
DR	EMBL; AB091766; BAC77075.1; -.
DR	MGD; MGI:2443411; B230315M08Rik.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0003677; C:DNA binding; IEA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR001005; Myb_DNA_binding.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
DR	PROSITE; PS00037; MYB_1; 1.
KW	SIGNAL.
FT	SIGNAL 1 27 POTENTIAL.
FT	CHAIN 28 314 POTENTIAL.
SQ	SEQUENCE 318 AA; 35629 MW; 490EBD46A0A7C6 CRC64;
Query Match	24.3%; Score 364; DB 11; Length 318;
Best Local Similarity	34.1%; Pred. No. 3.6e-26;
Matches 108; Conservative	49; Mismatches 116; Indels 44; Gaps 11;
QY	1 MPLLTLLVLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKMWCRGAIWR 60
DB	10 LPTLLALLLFWLPG---CVPLHGPTMTSGSVCSLSVSCRTEEKFKTKYKWCRLK 66
QY	61 DKILVKTSGSEQVKKRDVSIKDNQKRTFTVTMEDLMKTADTWCIGIEKT--GNDLG 118
DB	67 LCKDIVKTSSE-EARSGRVTRDHPDNLFTVTYESLTLEDADTYNCADVDSLFDGSLG 125
QY	119 VTQVTTIDPAPVTOEETSSSTPLT-----GHLDNRHKLKLS 156
DB	126 FDKYFKIELSVVPSDDPVSSPGPTEPVPVSTSLPTKGPALGSNTGHEHDYSQGLRLP 185
QY	157 VLLPLIFTIXLLLVAAASLLAWRMKYYQKAAAGSPS---QVLPLEGDLGVADLTQLA 213
DB	186 ALLS-VLALLFLVGTSLTLLAWRMFKRLVKADRHPELSQNLRAQSENECQY-VNLQLH 243
QY	214 GTSPKATTKLSSAQDVQVEVYVTVMASLPKEDISVASTLIGADDEPTYCNMGLSSXL 273
DB	244 TWSLRPEVLPVSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD--SHANGDSLH--- 294
QY	274 PGRGPEEPTTEYSTISRP 290
DB	295 --QPDQKAEYSEIQKP 309
RESULT 13	
Q8VCH2	PRELIMINARY; PRT; 221 AA.
ID	Q8VCH2
AC	Q8VCH2;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein.

Db	244 REBPVPSQVEV----	VEYSTLA-LPQELHYSSVAFNSQRQD--SHANGDSLH-----QP	292
QY	278 PEEPTTEYSTISRP	290	
Db	293 QDQKAEYSEIQKP	305	
RESULT 11			
Q7TN56	PRELIMINARY; PRT; 318 AA.		
AC	Q7TN56;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Mast cell-derived paired immunoglobulin-like receptor1.		
GN	MCP1R1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CBA/J;		
RC	MEDLINE=22774707; PubMed=12893283;		
RA	Kumagai H., Oki T., Tamitsu K., Feng S.-Z., Ono M., Nakajima H.,		
RA	Bao Y.-C., Kawakami Y., Nagayoshi K., Copeland N.G., Gilbert D.J.,		
RA	Jenkins N.A., Kawakami T., Kitamura T.;		
RT	"Identification and characterization of a new pair of immunoglobulin-		
RT	like receptors LIMR1 and 2 derived from murine bone marrow-derived		
RT	mast cells.";		
RL	Biochem. Biophys. Res. Commun. 307:719-729(2003).		
DR	EMBL; AB095675; BAC80268.1; -.		
KW	Receptor.		
SQ	SEQUENCE 318 AA; 35654 MW; E5DAB56711EA510 CRC64;		
Query Match	24.5%; Score 367; DB 11; Length 318;		
Best Local Similarity	34.4%; Pred. No. 1.9e-26;		
Matches 109; Conservative	50; Mismatches 114; Indels 44; Gaps 12;		
QY	1 MPLLTLLVLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKMWCRGAIWR 60		
DB	10 LPTLLALLLFWLPG---CVPLHGPTMTGVSQSLSVSQYEEKFKTKYKWCRLKV 66		
QY	61 DKILVKTSGSEQVKKRDVSIKDNQKRTFTVTMEDLMKTADTWCIGIEKT--GNDLG 118		
DB	67 LCKDIVKTSSE-EARSGRVTRDHPDNLFTVTYESLTLEDADTYNCADVDPFFNAPLG 125		
QY	119 VTQVTTIDPAPVTOEETSSSTPLT-----GHLDNRHKL-----LKL 156		
DB	126 LDKYFKIELSVVPSDDPVSSPGPTEPVPVSTSLPTKGPALGSNTEDREHDYSQGLRLP 185		
QY	157 VLLPLIFTIXLLLVAAASLLAWRMKYYQKAAAGSPS---QVLPLEGDLGVADLTQLA 213		
DB	186 ALLS-VLALLFLVGTSLTLLAWRMFKRLVKADRHPELSQNLRAQSENECQY-VNLQLH 243		
QY	214 GTSPKATTKLSSAQDVQVEVYVTVMASLPKEDISVASTLIGADDEPTYCNMGLSSXL 273		
DB	244 TWSLRPEVLPVSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD--SHANGDSLH--- 294		
QY	274 PGRGPEEPTTEYSTISRP 290		
DB	295 --QPDQKAEYSEIQKP 309		
RESULT 12			
Q8CFN3	PRELIMINARY; PRT; 318 AA.		
ID	Q8CFN3;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	MMAC8 precursor (MAIR-Ib).		
QY	1 MPLLTLLVLLFWLSGYSIATQITGPTTVNGLRSGSLTVQCVYRSGWETYLKMWCRGAIWR 60		
DB	10 LPTLLALLLFWLPG---CVPLHGPTMTGVSQSLSVSQYEEKFKTKYKWCRLKV 66		
QY	61 DKILVKTSGSEQVKKRDVSIKDNQKRTFTVTMEDLMKTADTWCIGIEKT--GNDLG 118		
DB	67 LCKDIVKTSSE-EARSGRVTRDHPDNLFTVTYESLTLEDADTYNCADVDPFFNAPLG 125		
QY	119 VTQVTTIDPAPVTOEETSSSTPLT-----GHLDNRHKL-----LKL 156		
DB	126 LDKYFKIELSVVPSDDPVSSPGPTEPVPVSTSLPTKGPALGSNTEDREHDYSQGLRLP 185		
QY	157 VLLPLIFTIXLLLVAAASLLAWRMKYYQKAAAGSPS---QVLPLEGDLGVADLTQLA 213		
DB	186 ALLS-VLALLFLVGTSLTLLAWRMFKRLVKADRHPELSQNLRAQSENECQY-VNLQLH 243		
QY	214 GTSPKATTKLSSAQDVQVEVYVTVMASLPKEDISVASTLIGADDEPTYCNMGLSSXL 273		
DB	244 TWSLRPEVLPVSQVEV---VEYSTLA-LPQELHYSSVAFNSQRQD--SHANGDSLH--- 294		
QY	274 PGRGPEEPTTEYSTISRP 290		
DB	295 --QPDQKAEYSEIQKP 309		

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GN 4732429D16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019814; AAHL9814.1; -.
DR MGD; MGI:2442358; 4732429D16RIK.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG.
DR SMART; SM00409; IG.
DR PROSITE; PS00038; HLH_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 221 AA; 24954 MW; C9E6203BE64922C1 CRC64;

Query Match 23.9%; Score 358.5; DB 11; Length 221;
Best Local Similarity 44.3%; Pred. No. 7.4e-26;
Matches 85; Conservative 21; Mismatches 65; Indels 21; Gaps 3;

QY 8 LLLFWLSGYSTA-TQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWRDCKILV 66
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LLLFPLGCGCTAQSIVTGFEEVSGQESLTVQCRYSYWKYKYGWCRGVPQQRSCDILV 66
QY 67 KTSGEQVQRDRYSIKDNQKNRFTVTMEDLMKTDADTYWCGIEKTNGLGVTVQVTID 126
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 ETDKSEQLVKKRVSRIRDQDFIFTVTMEDLRMSDAGIYWCITKGGPDPMFKNVNIID 126
QY 127 PAPVTOETSSPTL-----TGHLDNRHK-----LLKSLVLLPLIPTIX 166
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 QAPKSSMMTTTATVLKSIQPSAENTGKEQVTSQSRPHRTSLSSIFLLMVFEVL 186
QY 167 LLLVVAASLLAW 178
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
187 PLLLSMLSAVLW 198

RESULT 15
QSUBK4 PRELIMINARY; PRT; 299 AA.
AC QSUBK4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE IRC1 (Leukocyte membrane antigen).
GN IRC1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA O'Connor C.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Cantoni C., Biassoni R.;
RT "Molecular cloning of a novel inhibitory receptor.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Cantoni C., Biassoni R.;
RT "IRCI isoforms.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224864; CAB55347.1; -.
DR EMBL; AJ010101; CAB52291.1; -.
DR EMBL; BC032352; AAH32352.1; -.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 299 AA; 33201 MW; 978461DA87E86269 CRC64;

Query Match 22.1%; Score 331; DB 4; Length 299;
Best Local Similarity 33.2%; Pred. No. 4.7e-23;
Matches 105; Conservative 52; Mismatches 101; Indels 58; Gaps 14;

QY 8 LLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVK 67
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LLLLMVPG---CFALSKCRVTAGVGGSLSVQCPYEKSHRTLNKYWCRRPQIFLDCDKIVE 63

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Db	64	TKGSAGK-RNGRVSIKQKQNRFTVTMEDLMKTDADTYWCGIE-----KTGNDLGVTVQV	122
Qy	124	TI-----DPAPVTOBETS-----SSPTL-----TGHLDNRHKL-----LKLSVL	158
Db	123	SVFPASTMTPASITAAKTSTITTAFFPPVSTTILFVAGATHSASIQEETEVEVNSQLPLL	182
Qy	159	LPLIFTIXLLLVAAASLLAWRMKYQOKAA-----GMSPEQVLOPLEGDLCYADLTQLA	213
Db	183	LSLL-ALLLLLVGASLLAWRMFKWIKAGDHSELSONPKQA--ATQSELHYANLELLMW	239
Qy	214	GTSRKAATKLSSAQVDQVEVEYVTMASLPKEDISYASLTILGAEDQDEPTYCNMGXLSXL	273
Db	240	PLQEKAPPR-----EVEVEYSTVAS-PREELHYASVVVDS-----NTNRIAAQR	283
Qy	274	PGRGPPEPTYSTISR	289
Db	284	P-REEPDSYVIRK	298

Search completed: September 16, 2004, 12:39:49
Job time : 119 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:41:16 ; Search time 122 Seconds
(without alignments)

671.629 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290
Sequence: 1 MPLLTYLLFLWLSGVSIAT.....SXLPGRGPPEPTFYSTISRP 290

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
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3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	166	57.2	290	4 AAB74712	Aab74712 Human mem
3	166	57.2	290	5 AAU83611	Aau83611 Human PRO
4	166	57.2	290	6 ABU80758	Abu80758 Human PRO
5	166	57.2	290	6 ABO33724	Abo33724 Novel hum
6	166	57.2	290	6 ABU82067	Abu82067 Novel hum
7	166	57.2	290	6 ABJ72247	Abj72247 Human PRO
8	166	57.2	290	6 ABJ72375	Abj72375 Human PRO
9	166	57.2	290	6 ABO34270	Abo34270 Human sec
10	166	57.2	290	7 ABJ72077	Abj72077 Human mem
11	166	57.2	290	7 ADB83530	Adb83530 Novel hum
12	166	57.2	290	7 ADB80636	Adb80636 Novel hum
13	166	57.2	290	7 ADB73177	Adb73177 Human hum
14	166	57.2	290	7 ADB78259	Adb78259 Novel hum
15	166	57.2	290	7 ADB84907	Adb84907 Human PRO
16	166	57.2	290	7 ADB78013	Adb78013 Novel hum
17	166	57.2	290	7 ADB87079	Adb87079 Human PRO
18	166	57.2	290	7 ADB84661	Adb84661 Human PRO
19	166	57.2	290	7 ADB83776	Adb83776 Novel hum
20	166	57.2	290	7 ADB72931	Adb72931 Novel hum
21	166	57.2	290	7 ADC36769	Adc36769 Human PRO
22	166	57.2	290	7 ADC21759	Adc21759 Human PRO
23	166	57.2	290	7 ADC49790	Adc49790 Novel hum
24	166	57.2	290	7 ADC48989	Adc48989 Novel hum
25	166	57.2	290	7 ADC49506	Adc49506 Novel hum

26	166	57.2	290	7 ADC47367	Adc47367 Novel hum
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36	166	57.2	290	8 ADC48743	Adc48743 Novel hum
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52	166	57.2	290	8 ADD74003	Add74003 Human PRO
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54	166	57.2	290	8 ADD75979	Add75979 Novel hum
55	166	57.2	290	8 ADD85471	Add85471 Novel hum
56	166	57.2	290	8 ADE05020	Ade05020 Human PRO
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58	166	57.2	290	8 ADD76777	Add76777 Novel hum
59	166	57.2	290	8 ADD86545	Add86545 Novel hum
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62	166	57.2	290	8 ADD77767	Add77767 Novel hum
63	166	57.2	290	8 ADD85225	Add85225 Novel hum
64	166	57.2	290	8 ADD73757	Add73757 Human PRO
65	166	57.2	290	8 ADD74495	Add74495 Human PRO
66	166	57.2	290	8 ADD77023	Add77023 Novel hum
67	166	57.2	290	8 ADD85717	Add85717 Novel hum
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69	166	57.2	290	8 ADD74741	Add74741 Human PRO
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72	149	51.4	244	7 ADB65051	Adb65051 Human PRO
73	128	44.1	305	4 AAU14520	Aau14520 Human nov
74	128	44.1	305	4 AAB66271	Aab66271 Human TAN
75	128	44.1	305	5 AAU08796	Aau08796 Human leu
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91	10	3.4	195	2 AAU99071	Aau99071 Partial h
92	10	3.4	201	2 AAU99070	Aau99070 Human PIG
93	10	3.4	201	4 AAU29327	Aau29327 Human PRO
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95	10	3.4	201	4 AAB31568	Aab31568 Amino aci
96	10	3.4	201	5 ABB84988	Abb84988 Human PRO
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98	10	3.4	201	6 ABU58703	Abu58703 Human PRO

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100	10	3.4	201	6	ABU84566	Abu84566	Human sec	173	10	3.4	201	6	ABU82473	Abu82473	Novel hum
101	10	3.4	201	6	ABR66440	Abu66440	Human sec	174	10	3.4	201	6	ABU87484	Abu87484	Human PRO
102	10	3.4	201	6	ABR65830	Abu65830	Human sec	175	10	3.4	201	6	ABU83956	Abu83956	Human sec
103	10	3.4	201	6	ABR659770	Abu659770	Human sec	176	10	3.4	201	6	ABO08330	Abu08330	Human PRO
104	10	3.4	201	6	ABU83009	Abu83009	Human PRO	177	10	3.4	201	6	ABU82041	Abu82041	Novel hum
105	10	3.4	201	6	ABU90130	Abu90130	Novel hum	178	10	3.4	201	6	ABU66205	Abu66205	Novel hum
106	10	3.4	201	6	ABR68379	Abu68379	Human sec	179	10	3.4	201	6	ABR60034	Abu60034	Human sec
107	10	3.4	201	6	ABR69432	Abu69432	Novel hum	180	10	3.4	201	6	ABU94222	Abu94222	Novel hum
108	10	3.4	201	6	ABU92863	Abu92863	Human sec	181	10	3.4	201	6	ABO00095	Abu000095	Novel hum
109	10	3.4	201	6	ABO08940	Abu08940	Human sec	182	10	3.4	201	6	ABR66745	Abu66745	Human sec
110	10	3.4	201	6	ABO02992	Abu02992	Human sec	183	10	3.4	201	6	ABR91163	Abu91163	Human sec
111	10	3.4	201	6	ABR75146	Abu75146	Human sec	184	10	3.4	201	6	ABU94590	Abu94590	Human PRO
112	10	3.4	201	6	ABR94908	Abu94908	Human sec	185	10	3.4	201	6	ABU79472	Abu79472	Human PRO
113	10	3.4	201	6	ABU85881	Abu85881	Human PRO	186	10	3.4	201	6	ABU86801	Abu86801	Human sec
114	10	3.4	201	6	ABU99041	Abu99041	Novel hum	187	10	3.4	201	6	ABU87106	Abu87106	Novel hum
115	10	3.4	201	6	ABU98256	Abu98256	Novel hum	188	10	3.4	201	6	ABU94895	Abu94895	Human PRO
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117	10	3.4	201	6	ABU83655	Abu83655	Human PRO	190	10	3.4	201	6	ABR70571	Abu70571	Human sec
118	10	3.4	201	6	ABU86496	Abu86496	Human sec	191	10	3.4	201	6	ABU98736	Abu98736	Human sec
119	10	3.4	201	6	ABU67709	Abu67709	Human sec	192	10	3.4	201	6	ABR66135	Abu66135	Human sec
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122	10	3.4	201	6	ABR93045	Abu93045	Human sec	195	10	3.4	201	6	ABU96127	Abu96127	Human PRO
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125	10	3.4	201	6	ABO19109	Abu19109	Human sec	198	10	3.4	201	6	ABO09855	Abu09855	Human sec
126	10	3.4	201	6	ABR78530	Abu78530	Human sec	199	10	3.4	201	6	ABO11127	Abu11127	Human sec
127	10	3.4	201	6	ABU85266	Abu85266	Novel hum	200	10	3.4	201	6	ABR71181	Abu71181	Human sec
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129	10	3.4	201	6	ABO11737	Abu11737	Human sec	202	10	3.4	201	6	ABU91657	Abu91657	Human PRO
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132	10	3.4	201	6	ABU83651	Abu83651	Human sec	205	10	3.4	201	6	ABU80338	Abu80338	Human PRO
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265	10	3.4	201	6	ABO02687	AbO02687 Human sec	338	10	3.4	201	6	ABO21451	AbO21451 Human sec
266	10	3.4	201	6	ABR90858	AbR90858 Human sec	339	10	3.4	201	6	ABO22366	AbO22366 Human sec
267	10	3.4	201	6	ABR73926	AbR73926 Human sec	340	10	3.4	201	6	ABR96800	AbR96800 Human sec
268	10	3.4	201	6	ABO17178	AbO17178 Human sec	341	10	3.4	201	6	ABR85978	AbR85978 Human sec
269	10	3.4	201	6	ABR94603	AbR94603 Human sec	342	10	3.4	201	6	ABR99960	AbR99960 Human sec
270	10	3.4	201	6	ABR76110	AbR76110 Human sec	343	10	3.4	201	6	ABM00511	AbM00511 Human sec
271	10	3.4	201	6	ABR71486	AbR71486 Human sec	344	10	3.4	201	6	ABM00816	AbM00816 Human sec
272	10	3.4	201	6	ABR93383	AbR93383 Human sec	345	10	3.4	201	6	ABO29943	AbO29943 Human sec
273	10	3.4	201	6	ABR93688	AbR93688 Human sec	346	10	3.4	201	6	ABM23809	AbM23809 Human sec
274	10	3.4	201	6	ABR88113	AbR88113 Human sec	347	10	3.4	201	6	ABM29604	AbM29604 Human sec
275	10	3.4	201	6	ABO28113	AbO28113 Human sec	348	10	3.4	201	6	ABO38535	AbO38535 Human sec
276	10	3.4	201	6	ABO30248	AbO30248 Human sec	349	10	3.4	201	6	ABO45835	AbO45835 Human PRO
277	10	3.4	201	6	ABO33457	AbO33457 Human PRO	350	10	3.4	201	6	ABM20759	AbM20759 Human sec
278	10	3.4	201	6	ABM05145	AbM05145 Human sec	351	10	3.4	201	6	ADA81879	Ada81879 Human sec
279	10	3.4	201	6	ABM09105	AbM09105 Human sec	352	10	3.4	201	6	ABO16873	AbO16873 Human sec
280	10	3.4	201	6	ABO36705	AbO36705 Human sec	353	10	3.4	201	6	ABO18499	AbO18499 Human sec
281	10	3.4	201	6	ABO35790	AbO35790 Human PRO	354	10	3.4	201	6	ABO22926	AbO22926 Human PRO
282	10	3.4	201	6	ABO39755	AbO39755 Human sec	355	10	3.4	201	6	ABO23231	AbO23231 Human PRO
283	10	3.4	201	6	ABM10630	AbM10630 Human sec	356	10	3.4	201	6	ABR92773	AbR92773 Human sec
284	10	3.4	201	6	ABM12155	AbM12155 Human sec	357	10	3.4	201	6	ABR81730	AbR81730 Human sec
285	10	3.4	201	6	ABO52301	AbO52301 Human PRO	358	10	3.4	201	6	ABM78154	AbM78154 Human sec
286	10	3.4	201	6	ABO52606	AbO52606 Human PRO	359	10	3.4	201	6	ABR89943	AbR89943 Human sec
287	10	3.4	201	6	ABO23924	AbO23924 Human sec	360	10	3.4	201	6	ABM26859	AbM26859 Human sec
288	10	3.4	201	6	ABR97410	AbR97410 Human sec	361	10	3.4	201	6	ABM13985	AbM13985 Human sec
289	10	3.4	201	6	ABR87198	AbR87198 Human sec	362	10	3.4	201	6	ABO28723	AbO28723 Human sec
290	10	3.4	201	6	ABM11240	AbM11240 Human sec	363	10	3.4	201	6	ABO30553	AbO30553 Human sec
291	10	3.4	201	6	ABM28384	AbM28384 Human sec	364	10	3.4	201	6	ABM07580	AbM07580 Human sec
292	10	3.4	201	6	ABO32383	AbO32383 Human sec	365	10	3.4	201	6	ABM04171	AbM04171 Human sec
293	10	3.4	201	6	ABM15510	AbM15510 Human sec	366	10	3.4	201	6	ABO37315	AbO37315 Human sec
294	10	3.4	201	6	ABM06665	AbM06665 Human sec	367	10	3.4	201	6	ABO41890	AbO41890 Human sec
295	10	3.4	201	6	ABM04476	AbM04476 Human sec	368	10	3.4	201	6	ABO35485	AbO35485 Human PRO
296	10	3.4	201	6	ABM22589	AbM22589 Human sec	369	10	3.4	201	6	ABM25334	AbM25334 Human sec
297	10	3.4	201	6	ABM07885	AbM07885 Human sec	370	10	3.4	201	6	ABO47726	AbO47726 Human sec
298	10	3.4	201	6	ABO40975	AbO40975 Human sec	371	10	3.4	201	6	ABO48031	AbO48031 Human sec
299	10	3.4	201	6	ABM35622	AbM35622 Human sec	372	10	3.4	201	6	ABO48841	AbO48841 Human sec
300	10	3.4	201	6	ABM33385	AbM33385 Human sec	373	10	3.4	201	6	ABO51691	AbO51691 Human PRO
301	10	3.4	201	6	ABO52911	AbO52911 Human PRO	374	10	3.4	201	6	ABO51996	AbO51996 Human PRO
302	10	3.4	201	6	ABO50471	AbO50471 Human sec	375	10	3.4	201	6	ABO50776	AbO50776 Human sec
303	10	3.4	201	6	ABU99465	AbU99465 Human sec	376	10	3.4	201	6	ABR79900	AbR79900 Human sec
304	10	3.4	201	6	ABO04517	AbO04517 Human sec	377	10	3.4	201	6	ABM17162	AbM17162 Human sec
305	10	3.4	201	6	ABR18687	AbR18687 Human sec	378	10	3.4	201	6	ABO18194	AbO18194 Human sec
306	10	3.4	201	6	ABR97715	AbR97715 Human sec	379	10	3.4	201	6	ABO21146	AbO21146 Human sec
307	10	3.4	201	6	ABR80815	AbR80815 Human sec	380	10	3.4	201	6	ABR97105	AbR97105 Human sec
308	10	3.4	201	6	ABM01426	AbM01426 Human sec	381	10	3.4	201	6	ABM12460	AbM12460 Human sec
309	10	3.4	201	6	ABR89028	AbR89028 Human sec	382	10	3.4	201	6	ABM16552	AbM16552 Human sec
310	10	3.4	201	6	ABM13680	AbM13680 Human sec	383	10	3.4	201	6	ABM24419	AbM24419 Human sec
311	10	3.4	201	6	ABM21064	AbM21064 Human sec	384	10	3.4	201	6	ABM14900	AbM14900 Human sec
312	10	3.4	201	6	ABO42195	AbO42195 Human sec	385	10	3.4	201	6	ABM04781	AbM04781 Human sec
313	10	3.4	201	6	ABO42805	AbO42805 Human sec	386	10	3.4	201	6	ABM06970	AbM06970 Human sec
314	10	3.4	201	6	ABM10325	AbM10325 Human sec	387	10	3.4	201	6	ABM09410	AbM09410 Human sec
315	10	3.4	201	6	ABO38840	AbO38840 Human sec	388	10	3.4	201	6	ABO39450	AbO39450 Human sec
316	10	3.4	201	6	ABM33080	AbM33080 Human sec	389	10	3.4	201	6	ABM75715	AbM75715 Human sec
317	10	3.4	201	6	ABM22894	AbM22894 Human sec	390	10	3.4	201	6	ABM25639	AbM25639 Human sec

391	10	3.4	201	6	ABM20149	Human sec	464	10	3.4	201	7	ABM24724	Human sec
392	10	3.4	201	6	ABO47055	Human PRO	465	10	3.4	201	7	ABO29638	Human sec
393	10	3.4	201	6	ABO47360	Human PRO	466	10	3.4	201	7	ABO31468	Human sec
394	10	3.4	201	6	ABO47360	Human PRO	467	10	3.4	201	7	ABM14595	Human sec
395	10	3.4	201	6	ABR71791	Human sec	468	10	3.4	201	7	ABM10020	Human sec
396	10	3.4	201	6	ABR72401	Human sec	469	10	3.4	201	7	ABO39145	Human sec
397	10	3.4	201	6	ABR98740	Human sec	470	10	3.4	201	7	ABM34910	Human sec
398	10	3.4	201	6	ABO07110	Human sec	471	10	3.4	201	7	ABO51386	Human sec
399	10	3.4	201	6	ABR85063	Human sec	472	10	3.4	201	7	ABO04212	Human sec
400	10	3.4	201	6	ABR73621	Human sec	473	10	3.4	201	7	ABO10682	Human PRO
401	10	3.4	201	6	ABR76715	Human sec	474	10	3.4	201	7	ABR77925	Human sec
402	10	3.4	201	6	ABR73316	Human sec	475	10	3.4	201	7	ABR79135	Human sec
403	10	3.4	201	6	ABM18382	Human sec	476	10	3.4	201	7	ABO24229	Human sec
404	10	3.4	201	6	ABO20841	Human sec	477	10	3.4	201	7	ABR93993	Human sec
405	10	3.4	201	6	ABO25584	Human PRO	478	10	3.4	201	7	ABM02036	Human sec
406	10	3.4	201	6	ABO25889	Human PRO	479	10	3.4	201	7	ABM78459	Human sec
407	10	3.4	201	6	ABR94298	Human sec	480	10	3.4	201	7	ABR90248	Human sec
408	10	3.4	201	6	ABR80205	Human sec	481	10	3.4	201	7	ABM27774	Human sec
409	10	3.4	201	6	ABM11545	Human sec	482	10	3.4	201	7	ABM13375	Human sec
410	10	3.4	201	6	ABO33152	Human PRO	483	10	3.4	201	7	ABO32078	Human sec
411	10	3.4	201	6	ABO30858	Human sec	484	10	3.4	201	7	ABM14290	Human sec
412	10	3.4	201	6	ABO31163	Human sec	485	10	3.4	201	7	ABM08495	Human sec
413	10	3.4	201	6	ABM27469	Human sec	486	10	3.4	201	7	ABO40365	Human sec
414	10	3.4	201	6	ABM30214	Human sec	487	10	3.4	201	7	ABM74800	Human sec
415	10	3.4	201	6	ABM05750	Human sec	488	10	3.4	201	7	ABM33395	Human sec
416	10	3.4	201	6	ABM15815	Human sec	489	10	3.4	201	7	ABM20454	Human sec
417	10	3.4	201	6	ABM08800	Human sec	490	10	3.4	201	7	ABO48946	Human sec
418	10	3.4	201	6	ABO42500	Human sec	491	10	3.4	201	7	ABR73011	Human sec
419	10	3.4	201	6	ABO38230	Human sec	492	10	3.4	201	7	ABO15653	Human sec
420	10	3.4	201	6	ABO46140	Human PRO	493	10	3.4	201	7	ABR85368	Human sec
421	10	3.4	201	6	ABM66943	Human sec	494	10	3.4	201	7	ABO15348	Human sec
422	10	3.4	201	6	ABM20720	Human sec	495	10	3.4	201	7	ABO17483	Human sec
423	10	3.4	201	6	ABM19844	Human sec	496	10	3.4	201	7	ABM17772	Human sec
424	10	3.4	201	6	ABO49556	Human sec	497	10	3.4	201	7	ABR56673	Human sec
425	10	3.4	201	6	ABO49861	Human sec	498	10	3.4	201	7	ABM77239	Human sec
426	10	3.4	201	6	ADA78972	Human sec	499	10	3.4	201	7	ABO28418	Human sec
427	10	3.4	201	6	ABR88418	Human sec	500	10	3.4	201	7	ABM23199	Human sec
428	10	3.4	201	6	ABM27164	Human sec	501	10	3.4	201	7	ABM30519	Human sec
429	10	3.4	201	6	ABM03561	Human sec	502	10	3.4	201	7	ABM21979	Human sec
430	10	3.4	201	7	ABO40060	Human sec	503	10	3.4	201	7	ABM21574	Human sec
431	10	3.4	201	7	ABO50166	Human sec	504	10	3.4	201	7	ABM15205	Human sec
432	10	3.4	201	7	ABO51081	Human sec	505	10	3.4	201	7	ABO37010	Human sec
433	10	3.4	201	7	ABO05537	Human sec	506	10	3.4	201	7	ABO37620	Human sec
434	10	3.4	201	7	ABR74841	Human sec	507	10	3.4	201	7	ABM75410	Human sec
435	10	3.4	201	7	ABR77320	Human sec	508	10	3.4	201	7	ABM33690	Human sec
436	10	3.4	201	7	ABM18077	Human sec	509	10	3.4	201	7	ABO46445	Human PRO
437	10	3.4	201	7	ABR96128	Human sec	510	10	3.4	201	7	ABO46445	Human sec
438	10	3.4	201	7	ABO22061	Human sec	511	10	3.4	201	7	ABM32044	Human sec
439	10	3.4	201	7	ABO20231	Human sec	512	10	3.4	201	7	ABM31434	Human sec
440	10	3.4	201	7	ABO24534	Human sec	513	10	3.4	201	7	ABM32044	Human sec
441	10	3.4	201	7	ABR86283	Human sec	514	10	3.4	201	7	ABM32044	Human sec
442	10	3.4	201	7	ABM10935	Human sec	515	10	3.4	201	7	ABM32044	Human sec
443	10	3.4	201	7	ABM16934	Human sec	516	10	3.4	201	7	ABM32044	Human sec
444	10	3.4	201	7	ABR89638	Human sec	517	10	3.4	201	7	ABM32044	Human sec
445	10	3.4	201	7	ABM12765	Human sec	518	10	3.4	201	7	ABM31129	Human sec
446	10	3.4	201	7	ABM06055	Human sec	519	10	3.4	201	7	ADD06081	Human sec
447	10	3.4	201	7	ABO35180	Human PRO	520	10	3.4	201	7	ADD06081	Human sec
448	10	3.4	201	7	ABM03256	Human sec	521	10	3.4	201	7	ADD06081	Human sec
449	10	3.4	201	7	ABM15234	Human sec	522	10	3.4	201	7	ADD06081	Human sec
450	10	3.4	201	7	ABM19539	Human sec	523	10	3.4	201	7	ADD06081	Human sec
451	10	3.4	201	7	ABO46750	Human PRO	524	10	3.4	201	8	ABM32044	Human sec
452	10	3.4	201	7	ABO49251	Human sec	525	10	3.4	201	8	ABM32044	Human sec
453	10	3.4	201	7	ABR69294	Human sec	526	10	3.4	201	8	ABM32044	Human sec
454	10	3.4	201	7	ABR89333	Human sec	527	9	3.1	194	5	ABM32044	Human sec
455	10	3.4	201	7	ABR72706	Human sec	528	9	3.1	619	7	ABM32044	Human sec
456	10	3.4	201	7	ABR74536	Human sec	529	9	3.1	619	7	ABM32044	Human sec
457	10	3.4	201	7	ABO18804	Human sec	530	9	3.1	623	7	ABM32044	Human sec
458	10	3.4	201	7	ABR80510	Human sec	531	9	3.1	1102	6	ABM32044	Human sec
459	10	3.4	201	7	ABM01731	Human sec	532	8	2.8	37	2	ABM32044	Human sec
460	10	3.4	201	7	ABM02341	Human sec	533	8	2.8	48	3	ABM32044	Human sec
461	10	3.4	201	7	ABR87503	Human sec	534	8	2.8	48	3	ABM32044	Human sec
462	10	3.4	201	7	ABM13070	Human sec	535	8	2.8	48	3	ABM32044	Human sec
463	10	3.4	201	7	ABM30824	Human sec	536	8	2.8	49	3	ABM32044	Human sec

537	8	2.8	64	6	ADA56926	Ada56926 Human sec	610	7	2.4	107	3	AAB15813	Aab15813 Human che
538	8	2.8	64	5	ADA40776	Ada40776 Human sec	611	7	2.4	107	5	ABP65256	Abp65256 Hypoxia-r
539	8	2.8	65	2	AAU07904	Aau07904 Human sec	612	7	2.4	107	6	ABU57617	Abu57617 Different
540	8	2.8	80	6	ABU37115	Abj37115 NOVX prot	613	7	2.4	107	6	ABU57618	Abu57618 Different
541	8	2.8	93	6	ABU37116	Abj37116 NOVX prot	614	7	2.4	107	6	ABU67715	Abu67715 Human CXK
542	8	2.8	102	2	AAR70793	Aar70793 Gro-Beta/	615	7	2.4	107	7	ABO07349	Abc07349 Amino aci
543	8	2.8	103	6	ABJ37114	Abj37114 NOVX prot	616	7	2.4	107	7	ADC78819	Adc78819 Human PRO
544	8	2.8	103	6	ABJ37113	Abj37113 NOVX prot	617	7	2.4	109	4	AAO10848	Aao10848 Human POL
545	8	2.8	107	2	AAR23034	Aar23034 Human Gro	618	7	2.4	109	5	ABP33528	Abp33528 Human ORF
546	8	2.8	107	2	AAR20589	Aar20589 Human mac	619	7	2.4	115	2	AAU12637	Aau12637 Human 5'
547	8	2.8	107	2	AAR20529	Aar20529 Human mac	620	7	2.4	119	4	AAU32860	Aau32860 Novel hum
548	8	2.8	107	2	AAR20590	Aar20590 Human mac	621	7	2.4	120	4	AAU07542	Aau07542 Clone 99,
549	8	2.8	107	2	AAR20530	Aar20530 Human mac	622	7	2.4	120	7	ABO23587	Abc023587 Neisseria
550	8	2.8	107	2	AAR70794	Aar70794 Gro-Gamma	623	7	2.4	124	3	AAU64704	Aau64704 Human 5'
551	8	2.8	107	2	AAW96714	Aaw96714 Growth re	624	7	2.4	134	3	AAU43145	Aag43145 Arabidops
552	8	2.8	107	3	AAU15810	Aau15810 Human che	625	7	2.4	134	3	AAU15572	Aag15572 Arabidops
553	8	2.8	107	5	ABP65254	Abp65254 Hypoxia-r	626	7	2.4	136	4	AAU07237	Aau07237 1-aminocy
554	8	2.8	107	6	ABP96785	Abp96785 Human COP	627	7	2.4	143	3	AAU15571	Aag15571 Arabidops
555	8	2.8	107	6	ABU67716	Abu67716 Human CXK	628	7	2.4	143	3	AAU43144	Aag43144 Arabidops
556	8	2.8	107	6	ABU07350	Abu07350 Amino aci	629	7	2.4	143	5	ABG71687	Abg71687 Human mac
557	8	2.8	107	5	ABP31409	Abp31409 Human ORF	630	7	2.4	145	3	AAU23380	Aab23380 Yeast AGA
558	8	2.8	125	5	ABP1409	Abp1409 Human ORF	631	7	2.4	153	5	ABU51699	Abu51699 Helicobac
559	8	2.8	131	4	AAU25812	Aau25812 Human pro	632	7	2.4	161	5	ABO05752	Abc005752 Human G p
560	8	2.8	138	4	AAU75945	Aag75945 Human col	633	7	2.4	167	3	AAU43143	Aag43143 Arabidops
561	8	2.8	150	3	AAU57885	Aay57885 Human tra	634	7	2.4	167	3	AAU15570	Abg15570 Arabidops
562	8	2.8	195	3	AAU94880	Aay94880 Human pro	635	7	2.4	175	4	ABG03484	Abg03484 Novel hum
563	8	2.8	200	4	AAE02640	Aae02640 Human DNA	636	7	2.4	185	6	ABU37668	Abu37668 Protein e
564	8	2.8	292	5	AAO19224	Aao19224 Human IRC	637	7	2.4	185	6	ABU37260	Abu37260 Protein e
565	8	2.8	298	2	AAU24023	Aay24023 Human CMR	638	7	2.4	208	6	ABP80476	Abp80476 N. gonorr
566	8	2.8	301	2	AAU24022	Aay24022 Human dis	639	7	2.4	208	6	ABP79656	Abp79656 N. gonorr
567	8	2.8	313	4	AAE02639	Aae02639 Human DNA	640	7	2.4	217	4	AAU53543	Aau53543 Propionib
568	8	2.8	461	7	ADC64559	Adc64559 Trichodes	641	7	2.4	217	6	ABM50062	Abm50062 Propionib
569	8	2.8	472	6	ABB82660	Abb82660 N. puncti	642	7	2.4	218	3	AAU65681	Aay65681 C. elegan
570	8	2.8	475	7	ADC64556	Adc64556 Nostoc pu	643	7	2.4	229	4	AAU04888	Aau04888 Micromono
571	8	2.8	475	6	ABB82659	Abb82659 Anabaena	644	7	2.4	235	4	ABR00941	Abu00941 Gene 216
572	8	2.8	475	7	ADC64555	Adc64555 Anabaena	645	7	2.4	235	6	ABR57160	Abu57160 Human p10
573	8	2.8	475	7	ADC64555	Adc64555 Anabaena	646	7	2.4	235	6	ABR55869	Abu55869 Human gen
574	7	2.4	29	6	AAO27002	Aao27002 Human NGR	647	7	2.4	236	6	ABU55867	Abu55867 Human gen
575	7	2.4	29	3	AAU54386	Aay54386 Amino aci	648	7	2.4	236	6	ABU55867	Abu55867 Human gen
576	7	2.4	30	3	AAU54395	Aay54395 Amino aci	649	7	2.4	255	4	ABG06508	Abg06508 Novel hum
577	7	2.4	31	3	AAU54387	Aay54387 Amino aci	650	7	2.4	257	6	ABD07794	Abd07794 Alloloco
578	7	2.4	31	3	AAU54388	Aay54388 Amino aci	651	7	2.4	266	4	AAU63702	Aab63702 Human gas
579	7	2.4	31	3	AAU54404	Aay54404 Amino aci	652	7	2.4	276	4	AAU63704	Aab63704 Human gas
580	7	2.4	32	3	AAU54396	Aay54396 Amino aci	653	7	2.4	286	3	AAU21001	Aag21001 Arabidops
581	7	2.4	32	3	AAU54389	Aay54389 Amino aci	654	7	2.4	299	3	AAU52488	Aas52488 Helicobac
582	7	2.4	32	3	AAU54405	Aay54405 Amino aci	655	7	2.4	299	5	ABU51909	Abu51909 Helicobac
583	7	2.4	32	3	AAU54397	Aay54397 Amino aci	656	7	2.4	302	4	ABR00940	Abu00940 Gene 216
584	7	2.4	33	3	AAU74959	Aaw74959 Human sec	657	7	2.4	302	6	ABU55868	Abu55868 Human gen
585	7	2.4	33	3	AAU54406	Aay54406 Amino aci	658	7	2.4	309	6	AAU26367	Aaw26367 Staphyloc
586	7	2.4	33	3	AAU54398	Aay54398 Amino aci	659	7	2.4	311	5	ABU50336	Abu50336 Helicobac
587	7	2.4	33	5	ABG95419	Abg95419 Human nov	660	7	2.4	311	5	ABU18975	Abj18975 Pathogen
588	7	2.4	33	6	ABO34613	Abo34613 Region of	661	7	2.4	312	4	AAU78884	Aam78884 Human pro
589	7	2.4	34	3	AAU54391	Aay54391 Amino aci	662	7	2.4	312	6	ABU72349	Abm72349 Staphyloc
590	7	2.4	34	3	AAU54399	Aay54399 Amino aci	663	7	2.4	313	6	ABF75549	Abp75549 Human sec
591	7	2.4	34	3	AAU54407	Aay54407 Amino aci	664	7	2.4	319	5	ABU55009	Abu55009 Lactococc
592	7	2.4	35	3	AAU54400	Aay54400 Amino aci	665	7	2.4	331	2	AAU42332	Aay42332 Staphyloc
593	7	2.4	35	3	AAU54408	Aay54408 Amino aci	666	7	2.4	331	2	AAU31825	Aay31825 Staphyloc
594	7	2.4	36	3	AAU54409	Aay54409 Amino aci	667	7	2.4	331	4	AAU90841	Aag90841 C glutami
595	7	2.4	42	3	AAU28732	Aab28732 Human sec	668	7	2.4	340	4	AAU73051	Abm73051 Staphyloc
596	7	2.4	50	5	AAU63141	Aau63141 Propionib	669	7	2.4	340	4	AAU31599	Aab31599 Amino aci
597	7	2.4	50	5	ABP34982	Abp34982 Human ORF	670	7	2.4	361	6	AAU78883	Aam78883 Human pro
598	7	2.4	50	6	ABM59660	Abm59660 Propionib	671	7	2.4	361	6	AAO30434	Aac30434 Human glu
599	7	2.4	59	4	ABE06114	Abe06114 Human gen	672	7	2.4	361	7	ABD07796	Abd07796 Alloloco
600	7	2.4	59	5	ABG33936	Abg33936 Human sec	673	7	2.4	361	7	ADD46622	Add46622 Human PRO
601	7	2.4	60	3	AAU87137	Aay87137 Human sec	674	7	2.4	363	3	AAU52168	Aas52168 Human sec
602	7	2.4	60	4	AAU01640	Aau01640 Human sec	675	7	2.4	373	7	ADC97421	Adc97421 E. faecili
603	7	2.4	92	1	AAP93591	Aap93591 Deduced s	676	7	2.4	388	2	AAU25698	Aau25698 Murine ad
604	7	2.4	92	2	AAW01805	Aaw01805 Murine m	677	7	2.4	391	6	ABO00918	Abc00918 Polypepti
605	7	2.4	92	2	AAU42166	Aay42166 Rat Mip1-	678	7	2.4	400	2	AAU32501	Aar32501 Beta-adre
606	7	2.4	105	5	AAU52436	Aam52436 HIV Nef1	679	7	2.4	400	2	AAU54992	Aar54992 Murine be
607	7	2.4	107	2	AAU70792	Aar70792 Melanoma	680	7	2.4	400	2	ADD47841	Add47841 Rat Prote
608	7	2.4	107	2	AAU96713	Aaw96713 Growth re	681	7	2.4	406	3	AAU21000	Aag21000 Arabidops
609	7	2.4	107	3	AAU15793	Aab15793 Human che	682	7	2.4	422	4	AAU82216	Aau82216 Megalomic

683	7	2.4	430	3	AG20999	Arabidops	756	7	2.4	704	4	AB82620	Mouse sub
684	7	2.4	434	6	AB20683	Protein e	757	7	2.4	744	4	AG78648	Human Rai
685	7	2.4	440	4	AB59628	Drosophil	758	7	2.4	746	2	AW80322	Bacillus
686	7	2.4	441	4	AM79867	Human pro	759	7	2.4	756	6	ABU39148	Protein e
687	7	2.4	441	4	AM79868	Human pro	760	7	2.4	759	2	AW46864	Bacillus
688	7	2.4	441	6	AC27001	Human NGR	761	7	2.4	759	2	AY24967	Bacillus
689	7	2.4	448	4	AM60715	Human bra	762	7	2.4	769	5	ABP68905	Human pol
690	7	2.4	448	4	AG55105	Human liv	763	7	2.4	769	7	AD56492	Human pro
691	7	2.4	448	5	ABG43242	Human pep	764	7	2.4	786	7	ADD43705	Bacillus
692	7	2.4	449	6	AAO19850	B licheni	765	7	2.4	787	3	AY59284	SUP toxin
693	7	2.4	449	6	AAO19851	B licheni	766	7	2.4	787	6	AB82567	B. thurin
694	7	2.4	470	4	AAU01085	Gene 7 Hu	767	7	2.4	787	6	AB82565	B. thurin
695	7	2.4	477	4	AB94878	Human pro	768	7	2.4	787	7	AD43701	Bacillus
696	7	2.4	477	4	AB94726	Human pro	769	7	2.4	788	7	AD07798	Rice prot
697	7	2.4	477	5	AAE15741	Human ami	770	7	2.4	788	7	ADD43703	Bacillus
698	7	2.4	478	6	ABU18317	Protein e	771	7	2.4	789	2	AA91244	B. thurin
699	7	2.4	491	5	AAU84364	Novel hum	772	7	2.4	789	2	AA91243	B. thurin
700	7	2.4	506	5	ABU51515	Helicobac	773	7	2.4	789	2	AAW19515	B. cereus
701	7	2.4	509	1	AP91060	Predicted	774	7	2.4	789	2	AAW19514	B. cereus
702	7	2.4	511	2	AAW4865	Bacillus	775	7	2.4	789	2	AAW80321	Bacillus
703	7	2.4	511	2	AAW4868	Bacillus	776	7	2.4	789	2	AAW80320	Bacillus
704	7	2.4	514	5	ABP70073	Human NOV	777	7	2.4	789	2	AAW60216	Bacillus
705	7	2.4	519	2	AAW35553	Protein i	778	7	2.4	789	2	AAW60217	Bacillus
706	7	2.4	521	2	AAW27808	Bovine he	779	7	2.4	789	2	AAW46726	Negative ve
707	7	2.4	521	2	AAW41344	Bovine he	780	7	2.4	789	2	AAW46725	Vegetativ
708	7	2.4	521	2	AAW77400	BHVI gIII	781	7	2.4	789	2	AAW46862	Bacillus
709	7	2.4	524	4	AB31600	Amino aci	782	7	2.4	789	2	AAW46870	Bacillus
710	7	2.4	524	5	AB309661	Amino aci	783	7	2.4	789	2	AAW46863	Bacillus
711	7	2.4	524	5	AB309663	Amino aci	784	7	2.4	789	2	AAW46868	Bacillus
712	7	2.4	530	4	AAW64386	Amino aci	785	7	2.4	789	2	AAW46867	Bacillus
713	7	2.4	533	4	AAW96234	Putative	786	7	2.4	789	2	AAW46866	Bacillus
714	7	2.4	547	4	ABW68141	Drosophil	787	7	2.4	789	2	AAW46861	Bacillus
715	7	2.4	560	7	ADD48908	Rat Prote	788	7	2.4	789	2	AAW46861	Bacillus
716	7	2.4	561	5	AB557090	Mouse isc	789	7	2.4	789	2	AY24971	Bacillus
717	7	2.4	564	2	AAW28413	Prod. of	790	7	2.4	789	2	AY24966	Bacillus
718	7	2.4	564	2	AAW69733	Cyclic-GM	791	7	2.4	789	2	AY24970	Bacillus
719	7	2.4	564	2	AAW11257	Heart cal	792	7	2.4	789	2	AY24974	Bacillus
720	7	2.4	564	2	AAW18041	Human hea	793	7	2.4	789	2	AY24972	Bacillus
721	7	2.4	564	2	AAW171229	Human 61	794	7	2.4	789	2	AY24965	Bacillus
722	7	2.4	564	2	AAW77045	Human hea	795	7	2.4	789	2	AY24964	Bacillus
723	7	2.4	564	2	AAW60757	Amino aci	796	7	2.4	789	2	AY24973	Bacillus
724	7	2.4	564	3	AAW80990	Human 61	797	7	2.4	789	2	AY24969	Bacillus
725	7	2.4	564	6	ABU58729	Human 61k	798	7	2.4	789	6	AB82566	B. thurin
726	7	2.4	569	4	ABG13053	Novel hum	799	7	2.4	790	2	AAW60215	Bacillus
727	7	2.4	579	4	AAW93285	Human pro	800	7	2.4	790	2	AAW46872	Bacillus
728	7	2.4	580	5	AB977409	Novel hum	801	7	2.4	790	2	AAW46871	Bacillus
729	7	2.4	580	6	AB882675	Human A10	802	7	2.4	790	2	AY24975	Bacillus
730	7	2.4	599	7	ADC31234	Human nov	803	7	2.4	796	2	AY59275	Toxin tro
731	7	2.4	614	2	AAW20991	H. pylori	804	7	2.4	796	2	AY11696	LckSH3 do
732	7	2.4	623	4	AAW92236	C glutami	805	7	2.4	796	5	ABP68904	Human pol
733	7	2.4	625	4	AAW79455	Corynebac	806	7	2.4	801	4	ABG2463	S. epider
734	7	2.4	633	4	ABG07544	Novel hum	807	7	2.4	801	6	ABU42569	Protein e
735	7	2.4	634	2	AAW28412	Prod. CDN	808	7	2.4	808	5	ABP38260	Staphyloc
736	7	2.4	634	2	AAW69732	Cyclic-GM	809	7	2.4	809	2	AAW91261	VIP3A(a)
737	7	2.4	634	2	AAW11256	Hippocamp	810	7	2.4	809	2	AAW19521	B. cereus
738	7	2.4	634	2	AAW18040	Human bra	811	7	2.4	809	2	AAW46732	Maize opt
739	7	2.4	634	2	AAW71228	Human 61	812	7	2.4	812	4	AAW47106	Second sp
740	7	2.4	634	2	AAW77044	Ca2+/calm	813	7	2.4	812	4	ABR00942	Gene 216
741	7	2.4	634	2	AAW60756	Amino aci	814	7	2.4	812	5	ABW78300	Amino aci
742	7	2.4	634	3	AAW80989	Human 61k	815	7	2.4	812	5	AAO14377	Human met
743	7	2.4	634	6	ABU58728	Human 61k	816	7	2.4	812	5	AAU98885	Human pro
744	7	2.4	634	7	ADE54788	Rat Prote	817	7	2.4	812	6	ABU55870	Human 216
745	7	2.4	634	7	ADE54792	Rat Prote	818	7	2.4	813	6	ABU29256	Human PRO
746	7	2.4	635	2	AAW75855	Human sec	819	7	2.4	813	6	ABU58632	Human PRO
747	7	2.4	635	2	AAW45160	Human sec	820	7	2.4	813	6	ABU8180	Novel hum
748	7	2.4	635	3	AAW71060	Human mem	821	7	2.4	813	6	ABU44495	Human sec
749	7	2.4	635	6	ABP97203	Tumour-as	822	7	2.4	813	6	ABR66369	Human sec
750	7	2.4	635	7	ADE54790	Human PRO	823	7	2.4	813	6	ABR65759	Human sec
751	7	2.4	635	7	ADE54794	Human PRO	824	7	2.4	813	6	ABU96699	Human PRO
752	7	2.4	651	4	ABG06511	Novel hum	825	7	2.4	813	6	ABU82338	Human PRO
753	7	2.4	652	4	ABW59286	Drosophil	826	7	2.4	813	6	ABU90059	Novel hum
754	7	2.4	661	4	ABW59862	Drosophil	827	7	2.4	813	6	ABW68308	Human sec
755	7	2.4	686	5	AAO14360	Human met	828	7	2.4	813	6	ABU96361	Novel hum

975 7 2.4 813 6 ABM07204 Human sec
976 7 2.4 813 6 ABM21298 Human sec
977 7 2.4 813 6 ABM09644 Human sec
978 7 2.4 813 6 ABO41514 Human sec
979 7 2.4 813 6 ABO36329 Human PRO
980 7 2.4 813 6 ABO43858 Human PRO
981 7 2.4 813 6 ABM76558 Human sec
982 7 2.4 813 6 ABM76254 Human sec
983 7 2.4 813 6 ABM25873 Human sec
984 7 2.4 813 6 ABM26178 Human sec
985 7 2.4 813 6 ABO03531 Human sec
986 7 2.4 813 6 ABO02616 Human sec
987 7 2.4 813 6 ABR90787 Human sec
988 7 2.4 813 6 ABR73855 Human sec
989 7 2.4 813 6 ABO17107 Human sec
990 7 2.4 813 6 ABR94532 Human sec
991 7 2.4 813 6 ABR76039 Human sec
992 7 2.4 813 6 ABR71415 Human sec
993 7 2.4 813 6 ABR93312 Human sec
994 7 2.4 813 6 ABR93617 Human sec
995 7 2.4 813 6 ABR88042 Human sec
996 7 2.4 813 6 ABO28042 Human sec
997 7 2.4 813 6 ABO30177 Human sec
998 7 2.4 813 6 ABO33386 Human PRO
999 7 2.4 813 6 ABM05074 Human sec
1000 7 2.4 813 6 ABM09034 Human sec

ALIGNMENTS

RESULT 1
AAB32379
ID AAB32379 standard; protein; 291 AA.

AC AAB32379;
XX
DT 16-JAN-2001 (first entry)
XX

XX Human secreted protein sequence encoded by gene 9 SEQ ID NO:65.

XX Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
KW cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
KW antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
KW antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
KW autoimmune disease; haematopoietic cell disorder; blood protein disorder;
KW agammaglobulinaemia; hyperproliferative disease; Gaucher's disease;
KW cardiovascular disorder; congenital heart defect; pulmonary atresia;
KW arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
KW atherosclerosis; neurological disease; Alzheimer's disease; Huntington's;
KW infectious disease; cat-scratch disease.

XX Homo sapiens.

XX WO200047602-A1.

XX 17-AUG-2000.

XX 08-FEB-2000; 2000WO-US0003062.

XX 10-FEB-1999; 99US-0119468P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR;

PI Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;

XX WPI; 2000-543578/49.

XX N-PSDB; AAC55198.

XX New human nucleic acids encoding secreted proteins, useful in the
PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
PT diseases), blood protein disorders and hyperproliferative diseases (e.g.

PT Gaucher's disease).

XX Claim 11; Page 428-429; 488pp; English.

XX The polynucleotide sequences given in AAC55190 to AAC55235 encode the
CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: cytostatic; immunostimulant
CC ; antiproliferative; cardiant; antiarrhythmic; antiviral; antibacterial;
CC antifungal; antiparasitic; neuroprotective; nootropic; antiinflammatory;
CC antiangiogenic; anti-HIV; and antiarteriosclerotic. The polynucleotides
CC and polypeptides, or their agonists and antagonists, can be used for
CC treating, preventing or diagnosing immune disorders (e.g. cancer,
CC autoimmune diseases), disorders of haematopoietic cells, blood protein
CC disorders (e.g. agammaglobulinaemia), hyperproliferative diseases (e.g.
CC Gaucher's disease), cardiovascular disorders (e.g. congenital heart
CC defects, pulmonary atresia, arrhythmias, ischaemia), angiogenesis related
CC disorders (e.g. Crohn's disease, atherosclerosis), neurological diseases
CC (e.g. Alzheimer's disease, Huntington's chorea), infectious diseases
CC (e.g. AIDS, cat-scratch disease and other bacterial, viral, parasitic or
CC fungal diseases). AAC55181 to AAC55189 and AAB32370 represent sequences
CC used in the exemplification of the present invention

XX Sequence 291 AA;

Query Match 99.0%; Score 287; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 8.4e-275;

Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLITLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCGRGAIWR 60

DB 1 MPLITLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCGRGAIWR 60

QY 61 DCKILVKTSGSEQVEKRDVSIKDNQKNRFTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

DB 61 DCKILVKTSGSEQVEKRDVSIKDNQKNRFTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

QY 121 VQVITDPAVTVQETSSPTLTGHLDNRHKLKLSVLPLIFITXILLVVAASLLAWRM 180

DB 121 VQVITDPAVTVQETSSPTLTGHLDNRHKLKLSVLPLIFITXILLVVAASLLAWRM 180

QY 181 MKYQQAAGMSPEQVLOPLEGDLQYADLTQLACTSPRKATTKLSSAQVDQVEVEYVTMA 240

DB 181 MKYQQAAGMSPEQVLOPLEGDLQYADLTQLACTSPRKATTKLSSAQVDQVEVEYVTMA 240

QY 241 SLPKEDISYASLTLAGDQDEPTYCNMGXLSXLPGRGPEPTSTSRP 290

DB 241 SLPKEDISYASLTLAGDQDEPTYCNMGXLSXLPGRGPEPTSTSRP 290

RESULT 2

AAB74712

ID AAB74712 standard; protein; 290 AA.

XX AC AAB74712;

XX 12-JUN-2001 (first entry)

XX Human membrane associated protein MEMAP-18.

XX Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.

XX Homo sapiens.

XX WO200112662-A2.

XX 22-FEB-2001.

XX

PF 14-AUG-2000; 2000WO-US022315.
XX 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn WE, Lu DAM, Patterson C;
XX WPI; 2001-169860/17.
DR N-PSDB; AAF81758.
XX Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX Claim 1; Page 131-132; 173pp; English.
XX AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated with
CC MEMAP
XX
SQ Sequence 290 AA;
Query Match 57.2%; Score 166; DB 4; Length 290;
Best Local Similarity 99.68; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLERSLTVQCVYRSGWETYLKWCRCGAIWR 60
Qy 61 DCKILVKTSGSEQVKEDRVSIKDNQKNTFTVTMEDLMKTDADTYWCGIEKTDNLGVT 120
Db 61 DCKILVKTSGSEQVKEDRVSIKDNQKNTFTVTMEDLMKTDADTYWCGIEKTDNLGVT 120
Qy 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXILLVLAASLLAWRM 180
Db 121 VQVITDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTXILLVLAASLLAWRM 180
Qy 181 MKYQKAAGMSPQVLPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVYVWMA 240
Db 181 MKYQKAAGMSPQVLPLEGDLCYADLTQLAGTSRKAATTKLSSAQVDQVEVYVWMA 240
Qy 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQEPYCNMG 267

RESULT 3
ID AAU83611 standard; protein; 290 AA.
XX

AC AAU83611;
XX 08-MAY-2002 (first entry)
XX Human PRO protein, Seq ID No 40.
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX Homo sapiens.
XX WO200206288-A2.
XX 31-JAN-2002.
XX 29-JUN-2001; 2001WO-US021056.
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX (GETH) GENENTECH INC.
XX Baker KP, Deanovers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33555.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX Claim 1; Fig 40; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumors, especially lung
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
CC liver tumor. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have

CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 5; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLTLVLLFWLSGYSIATQITGTTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
Db 1 MLLTLVLLFWLSGYSIATQITGTTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 4

ABU80758
ID ABU80758 standard; protein; 290 AA.
AC ABU80758;
XX
XX
XX 23-JUN-2003 (first entry)
XX Human PRO polypeptide #20.
XX Human; PRO polypeptide; secreted and transmembrane protein;
XX anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX Homo sapiens.
XX US2003036635-A1.
XX
XX 20-FEB-2003.
XX
XX 28-AUG-2002; 2002US-00230163.
XX
XX 25-JUN-2000; 2000US-0220638P.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
XX N-PSDB; ACA66860.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for the manufacture of a medicament for diagnosing or treating
XX tumor.
XX
XX Claim 11; Fig 40; 314pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO

CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. AB080739-AB080860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDENTry.html
XX

SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLTLVLLFWLSGYSIATQITGTTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
Db 1 MLLTLVLLFWLSGYSIATQITGTTVNGLSLTVQCYVRSWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQQAAGMSPEQVLPLEGDLQVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 5

ABO33724
ID ABO33724 standard; protein; 290 AA.
XX
XX ABO33724;
XX
XX 17-SEP-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO10111.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic;
XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
XX pharmaceutical; diagnostic; biosensor; bioeffector; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; bone disorder; cartilage disorder; sports injury;
XX arthritis; wound.
XX Homo sapiens.
XX
XX US2003045687-A1.
XX
XX 06-MAR-2003.
XX
XX 12-AUG-2002; 2002US-00218631.
XX
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-512315/48.

DR N-PSDB; ACD58612.
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
PS Claim 11; Fig 40; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEGEVQRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKGTNDLGYT 120
Db 61 DCKILVKTSGSEGEVQRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKGTNDLGYT 120

QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180

QY 181 MKYQKAAAGMSPEQVLPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVYVTMA 240
Db 181 MKYQKAAAGMSPEQVLPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVYVTMA 240

RESULT 6
ABU82067
ID ABU82067 standard; protein; 290 AA.
XX
AC ABU82067;
XX
DT 25-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10111.
XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW

KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
XX US2003089063-A1.
XX
PD 08-MAY-2003.
XX
PF 12-AUG-2002; 2002US-00219003.
XX
XX 25-JUL-2000; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI
DR WPI; 2003-393229/37.
DR N-PSDB; ACA68516.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 40; 314pp; English.
XX
XX The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEGEVQRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKGTNDLGYT 120
Db 61 DCKILVKTSGSEGEVQRDRVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKGTNDLGYT 120

QY 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
Db 121 VQVTTIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180

QY 181 MKYQKAAAGMSPEQVLPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVYVTMA 240
Db 181 MKYQKAAAGMSPEQVLPLEGDLQYADLTQLAGTSPRKATTKLSSAQVDQVEVYVTMA 240

QY 241 SLPKEDISYASLTGAEDEQPTVCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTVCNMG 267

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RESULT 7
ABJ72247
ID ABJ72247 standard; protein; 290 AA.
XX
AC ABJ72247;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10111 protein.
XX
KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003050448-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230414.
XX
XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-521818/49.
DR N-PSDB; ABT44245.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX
PS Claim 11; Fig 40; 315pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, and the stimulation of human dermal fibroblast cell
CC proliferation, and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
XX protein of the invention
XX
SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYSGWETYLKWCRCGAIWR 60
QY 61 DCKILVTSGSEQVSKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNLDLGT 120
Db 61 DCKILVTSGSEQVSKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNLDLGT 120
QY 121 VQVTFIDPAPVQETSSPTLTGHHLNRRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
Db 121 VQVTFIDPAPVQETSSPTLTGHHLNRRHKLKLSVLLPLFTIXLLLLVAASLLAWRM 180
QY 181 MKYQQAAGMSPEQLQPLEGDLCLYADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240

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Db 181 MKYQQAAGMSPEQLQPLEGDLCLYADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGLGAEDQEPTYCNMG 267
XX
Db 241 SLPKEDISYASLTGLGAEDQEPTYCNMG 267
XX
RESULT 8
ABJ72375
ID ABJ72375 standard; protein; 290 AA.
XX
AC ABJ72375;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10111 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
XX tumour necrosis factor; proliferation; differentiation; gene therapy;
XX dermal fibroblast.
XX
OS Homo sapiens.
XX
PN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
XX 26-AUG-2002; 2002US-00227884.
PF
XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-503301/47.
DR N-PSDB; ABT44528.
XX
XX New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
PS Claim 11; Fig 40; 324pp; English.
XX
CC The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
SQ Sequence 290 AA;

Query Match 57.2%; Score 166; DB 6; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYSGWETYLKWCRCGAIWR 60
Db 1 MPLLTLVLLFWLSGYSIATQITGPTTVNGLSLTVQCVYSGWETYLKWCRCGAIWR 60
QY 61 DCKILVTSGSEQVSKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNLDLGT 120
Db 61 DCKILVTSGSEQVSKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTNLDLGT 120

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QY 121 VQVTDIPAPVQEBTSSPTLGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 DB 121 VQVTDIPAPVQEBTSSPTLGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLQVADLTQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPQLEGDLQVADLTQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 DB 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 RESULT 9
 ABO34270
 ID ABO34270 standard; protein; 290 AA.
 AC ABO34270;
 XX
 DT 19-SEP-2003 (first entry)
 DE Human secreted/transmembrane polypeptide PRO 10111.
 XX
 KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
 KW human dermal fibroblast stimulation; tumour; tissue typing;
 KW affinity purification.
 XX
 OS Homo sapiens.
 XX
 FN US2003044934-A1.
 XX
 PD 06-MAR-2003.
 XX
 PF 28-AUG-2002; 2002US-00230338.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-492274/46.
 DR N-PSDB; ACD82195.
 XX
 PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, or in generating probes.
 XX
 PS Claim 19; Fig 40; 315pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. Nucleic acids that encode PRO can be used to generate either
 CC transgenic animals or knock-out animals useful in developing and
 CC screening of therapeutically useful reagents. The nucleic acids may also
 CC be used in gene therapy for replacing defective gene, in chromosome
 CC identification, as chromosome markers, or in generating probes to isolate
 CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
 CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
 CC and for detecting the presence of tumour in an animal. The PRO
 CC polypeptides are useful as molecular markers for protein electrophoresis
 CC and the isolated nucleic acids may be used for recombinantly expressing
 CC those markers. The PRO polypeptides and nucleic acids may also be used in
 CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
 CC PRO and in affinity purification of PRO from recombinant cell culture or
 CC natural sources. The present sequence represents the amino acid sequence
 CC of a human secreted/transmembrane PRO polypeptide
 XX
 SQ Sequence 290 AA;
 Query Match 57.2%; Score 166; DB 6; Length 290;

Best Local Similarity 99.6%; Pred. No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPELLTYLLFWLSGYSIATQITGTTVNGLERGLSTVQCVRSGWETYLKWCRCGAIWR 60
 DB 1 MPELLTYLLFWLSGYSIATQITGTTVNGLERGLSTVQCVRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVKTSSGEQVRKDRVSIKDNQKRIFTVTMEDLMKTDADTYWCGIEKTDGNDIGVT 120
 DB 61 DCKILVKTSSGEQVRKDRVSIKDNQKRIFTVTMEDLMKTDADTYWCGIEKTDGNDIGVT 120
 QY 121 VQVTDIPAPVQEBTSSPTLGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 DB 121 VQVTDIPAPVQEBTSSPTLGHLDNRHKLKLSVLLPLIFTXLLLLVAASLLAWRM 180
 QY 181 MKYQQAAGMSPEQVLPQLEGDLQVADLTQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 DB 181 MKYQQAAGMSPEQVLPQLEGDLQVADLTQAGTSPRKATTKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 DB 241 SLPKEDISYASLTGAEDEQPTCYNMG 267
 RESULT 10
 ABU72077
 ID ABU72077 standard; protein; 290 AA.
 AC ABU72077;
 XX
 DT 16-OCT-2003 (first entry)
 DE Human membrane bound receptor/protein PRO10111 amino acid sequence.
 XX
 KW Human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuroepithelial; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX
 OS Homo sapiens.
 XX
 FN US2003065147-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 29-AUG-2002; 2002US-00232224.
 XX
 PR 28-JUL-1999; 99US-0146222P.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-522018/49.
 DR N-PSDB; ABT43901.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides;
 PT useful for the manufacture of a medicament for diagnosing or treating
 PT tumor.
 XX
 PS Claim 11; Fig 40; 315pp; English.
 XX
 CC This invention relates to one hundred and twenty two novel nucleic acids
 CC encoding human PRO membrane bound proteins or receptors. Extracellular
 CC proteins play important roles in the formation, differentiation and
 CC maintenance of multicellular organisms. The fate of many individual cells

(for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor -ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention

XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 7; Length 290;
Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60

Qy 61 DCKILVKTSGSEQVKKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQVKKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

Qy 121 VQVTDIDPAPVQTEETSSPTLTGHLDNRHKLKLSVLLPIFTIIXLLLVAAASLLAWRM 180
Db 121 VQVTDIDPAPVQTEETSSPTLTGHLDNRHKLKLSVLLPIFTIIXLLLVAAASLLAWRM 180

Qy 181 MKYQKKAAGMSPEQVLPLEGDLQADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
Db 181 MKYQKKAAGMSPEQVLPLEGDLQADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

Qy 241 SLPKEDISYASLTGAEQDQPTVCNMG 267
Db 241 SLPKEDISYASLTGAEQDQPTVCNMG 267

RESULT 11

ID ADB83530 standard; protein; 290 AA.

AC ADB83530;

DT 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10111.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.

XX Homo sapiens.

XX US2003073814-A1.

XX 17-APR-2003.

XX 12-AUG-2002; 2002US-00218849.

XX

PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WPI; 2003-644806/61.
XX N-PSDB; ADB83529.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX in gene therapy, chromosome identification, tissue typing, or as
XX hybridization probes in chromosome and gene mapping.

XX Claim 11; Fig 40; 315pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO331, PRO357, PRO725, PRO1155, PRO1366 or PRO1419 polypeptide
XX are useful for stimulating the release of tumour necrosis factor (TNF) -
XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
XX PRO1478, PRO1134, PRO836, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
XX PRO1286, PRO1330, PRO1447, PRO1385, PRO1273, PRO1340, PRO1338,
XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1317, PRO1760, PRO1587,
XX PRO1887, PRO1928, PRO1341, PRO1801, PRO4333, PRO3543, PRO15322,
XX PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX stimulating the proliferation of normal human dermal fibroblasts cells.
XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc.,
XX are useful for detecting the presence of expression of the above PRO polypeptides
XX in a test sample of cells taken from the mammal, and a control sample of
XX normal cells of the same cell type, where a higher level of expression of
XX the PRO polypeptides in the test sample as compared to the control sample
XX is indicative of the presence of tumour in the mammal. The tumour is lung
XX tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. (I) is useful as molecular weight markers, for tissue
XX typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
XX useful for chromosome and gene mapping or gene therapy. (II) is useful
XX for generating transgenic animals or knock-out animals which are useful
XX screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
XX is useful for treating bone and/or cartilage disorders (e.g., arthritis,
XX sport injuries). This is the amino acid sequence of a human secreted and
XX transmembrane PRO polypeptide.

XX Sequence 290 AA;

Query Match 57.2%; Score 166; DB 7; Length 290;

Best Local Similarity 99.6%; Pred. No. 3.3e-155;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSGWETYLKWCRCGAIWR 60

Qy 61 DCKILVKTSGSEQVKKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120
Db 61 DCKILVKTSGSEQVKKDRVSIKDNQKRTFTVMDLTKTDADTYWCGIEKTDGLVGT 120

Qy 121 VQVTDIDPAPVQTEETSSPTLTGHLDNRHKLKLSVLLPIFTIIXLLLVAAASLLAWRM 180
Db 121 VQVTDIDPAPVQTEETSSPTLTGHLDNRHKLKLSVLLPIFTIIXLLLVAAASLLAWRM 180

Qy 181 MKYQKKAAGMSPEQVLPLEGDLQADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQKAAAGSPQVLPLEGDLCLYADLTQLAGTSRKAATKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 12
 ADB80636
 ID ADB80636 standard; protein; 290 AA.
 AC ADB80636;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10111.
 XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 XX US2003088068-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 13-AUG-2002; 2002US-00219481.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-657982/62.
 XX N-PSDB; ADB80635.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 XX Claim 11; Fig 40; 305pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 290 AA;
 QY
 Query Match 57.2%; Score 166; DB 7; Length 290;
 Best Local Similarity 99.6%; Pred.No. 3.3e-155;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPLLTYLLLEFWLSGYSIATQITGPTTVNGLSGLTVQCVYRSGWETYLKWCRCGAIWR 60
 Db 1 MPLLTYLLLEFWLSGYSIATQITGPTTVNGLSGLTVQCVYRSGWETYLKWCRCGAIWR 60
 QY 61 DCKILVTSGSEQEVKDRVSIKONQKNRPTVTVMEDLMKTDADTYWCGIEKTDGLVLT 120
 Db 61 DCKILVTSGSEQEVKDRVSIKONQKNRPTVTVMEDLMKTDADTYWCGIEKTDGLVLT 120
 QY 121 VQVTDPAVPTQERTSSPTLTGHLNDRHKLKLSVLLPIFTIXLLLVAAISLLAWRM 180
 Db 121 VQVTDPAVPTQERTSSPTLTGHLNDRHKLKLSVLLPIFTIXLLLVAAISLLAWRM 180
 QY 181 MKYQKAAAGSPQVLPLEGDLCLYADLTQLAGTSRKAATKLSSAQVDQVEVEYVTMA 240
 Db 181 MKYQKAAAGSPQVLPLEGDLCLYADLTQLAGTSRKAATKLSSAQVDQVEVEYVTMA 240
 QY 241 SLPKEDISYASLTGAEDEPTCYNMG 267
 Db 241 SLPKEDISYASLTGAEDEPTCYNMG 267

RESULT 13
 ADB73177
 ID ADB73177 standard; protein; 290 AA.
 AC ADB73177;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10111.
 XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 XX US2003096968-A1.
 XX
 XX 22-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232223.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX

29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
(GETH) GENENTECH INC.
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
WPI: 2003-765525/72.
N-PSDB; ADB73176.
New isolated PRO polypeptides useful as molecular weight markers in
protein electrophoresis, useful for tissue typing, and for treating
arthritis and tumors.
Claim 11; Fig 40; 308pp; English.
The invention describes an isolated PRO (secreted and transmembrane)
polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (TNF)-
alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1412,
PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338,
PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
stimulating the proliferation of normal human dermal fibroblasts cells.
PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
inhibiting the proliferation of normal human dermal fibroblast cells. PRO
polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
are useful for detecting the presence of tumour in a mammal which
involves comparing the level of expression of the above PRO polypeptides
in a test sample of cells taken from the mammal, and a control sample of
normal cells of the same cell type, where a higher level of expression of
the PRO polypeptides in the test sample as compared to the control sample
is indicative of the presence of tumour in the mammal. The tumour is lung
tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
liver tumour. (I) is useful as molecular weight markers, for tissue
typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
useful for chromosome and gene mapping or gene therapy. (II) is useful
for generating transgenic animals or knock-out animals which are useful
screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
is useful for treating bone and/or cartilage disorders (e.g., arthritis,
sport injuries). This is the amino acid sequence of a human secreted and
transmembrane PRO polypeptide.

Query Match
Best Local Similarity 57.2%; Score 166; DB 7; Length 290;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MFLTLVLLFWLGSYGIATQITPTTVNGLGRSLTVQCVYRSGMETHYKWCGRGAINR 60
Db 1 MFLTLVLLFWLGSYGIATQITPTTVNGLGRSLTVQCVYRSGMETHYKWCGRGAINR 60
Qy 61 DCKILVTSQGEQVKRDRYSIKDNQNRFTVTMEDLMKTDADTYWCGIEKTNLDLGV 120
Db 61 DCKILVTSQGEQVKRDRYSIKDNQNRFTVTMEDLMKTDADTYWCGIEKTNLDLGV 120
Qy 121 VQVITDPAPVTQETSSPILTGHHLDNRHKLKLSVLLPLFTIILLVAASLLAWRM 180
Db 121 VQVITDPAPVTQETSSPILTGHHLDNRHKLKLSVLLPLFTIILLVAASLLAWRM 180
Qy 181 MKYQOKAAGSPQVQLPGLGDLVADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQOKAAGSPQVQLPGLGDLVADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
Qy 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQDEPTYCNMG 267
RESULT 14
ADB78259
ID ADB78259 standard; protein; 290 AA.
XX ADB78259;
XX DT 04-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10111.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
(TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
gene therapy.
XX KW Homo sapiens.
OS US2003092889-A1.
XX PD 15-MAY-2003.
XX FF 13-AUG-2002; 2002US-00219478.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-765495/72.
XX N-PSDB; ADB78258.
XX DR New isolated PRO polypeptide useful for tissue typing, gene therapy, as
XX molecular weight markers in protein electrophoresis, and for treating
XX arthritis and tumors.
XX Claim 11; Fig 40; 308pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
XX are useful for stimulating the release of tumour necrosis factor (TNF)-
XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1412,
XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338,
XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,
XX PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX stimulating the proliferation of normal human dermal fibroblasts cells.
XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:51:52 : Search time 32 Seconds
(without alignments)
467.860 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	3.4	195	3	US-08-955-937A-4
2	10	3.4	195	3	US-09-300-985-4
3	10	3.4	201	3	US-08-955-937A-2
4	10	3.4	201	3	US-09-300-985-2
5	8	2.8	107	1	US-08-352-324A-4
6	8	2.8	107	2	US-08-862-607-4
7	8	2.8	107	2	US-08-468-819-6
8	8	2.8	107	3	US-09-203-235-4
9	8	2.8	107	4	US-09-213-383-6
10	8	2.8	107	5	PCT-US95-16144-4
11	8	2.8	298	4	US-09-582-934-2
12	8	2.8	301	4	US-09-582-934-1
13	7	2.4	29	3	US-09-348-578-4
14	7	2.4	29	4	US-09-699-684-4
15	7	2.4	30	1	US-08-087-772A-9
16	7	2.4	30	3	US-09-348-578-13
17	7	2.4	30	4	US-09-699-684-5
18	7	2.4	30	4	US-09-699-684-13
19	7	2.4	31	3	US-09-348-578-6
20	7	2.4	31	3	US-09-348-578-14
21	7	2.4	31	3	US-09-348-578-22
22	7	2.4	31	4	US-09-699-684-6
23	7	2.4	31	4	US-09-699-684-14
24	7	2.4	31	4	US-09-699-684-22
25	7	2.4	32	3	US-09-348-578-7
26	7	2.4	32	3	US-09-348-578-15
27	7	2.4	32	3	US-09-348-578-15

28	7	2.4	32	3	US-09-348-578-23	Sequence 23, Appl
29	7	2.4	32	4	US-09-699-684-7	Sequence 7, Appl
30	7	2.4	32	4	US-09-699-684-15	Sequence 15, Appl
31	7	2.4	32	4	US-09-699-684-23	Sequence 23, Appl
32	7	2.4	33	3	US-09-348-578-8	Sequence 8, Appl
33	7	2.4	33	3	US-09-348-578-16	Sequence 16, Appl
34	7	2.4	33	3	US-09-348-578-24	Sequence 24, Appl
35	7	2.4	33	4	US-09-149-476-559	Sequence 559, App
36	7	2.4	33	4	US-09-699-684-8	Sequence 8, Appl
37	7	2.4	33	4	US-09-699-684-16	Sequence 16, Appl
38	7	2.4	33	4	US-09-699-684-24	Sequence 24, Appl
39	7	2.4	34	3	US-09-348-578-9	Sequence 9, Appl
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41	7	2.4	34	3	US-09-348-578-25	Sequence 25, Appl
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43	7	2.4	34	4	US-09-699-684-17	Sequence 17, Appl
44	7	2.4	34	4	US-09-699-684-25	Sequence 25, Appl
45	7	2.4	35	3	US-09-348-578-18	Sequence 18, Appl
46	7	2.4	35	4	US-09-348-578-26	Sequence 26, Appl
47	7	2.4	35	4	US-09-699-684-18	Sequence 18, Appl
48	7	2.4	35	4	US-09-699-684-26	Sequence 26, Appl
49	7	2.4	36	3	US-09-348-578-27	Sequence 27, Appl
50	7	2.4	36	4	US-09-699-684-27	Sequence 27, Appl
51	7	2.4	60	4	US-09-482-273-176	Sequence 176, App
52	7	2.4	92	4	US-09-195-106-3	Sequence 3, Appl
53	7	2.4	92	4	US-08-649-006A-9	Sequence 9, Appl
54	7	2.4	92	4	US-09-771-023-11	Sequence 11, Appl
55	7	2.4	106	4	US-08-679-493A-148	Sequence 148, App
56	7	2.4	107	1	US-08-352-324A-7	Sequence 7, Appl
57	7	2.4	107	2	US-08-862-607-7	Sequence 7, Appl
58	7	2.4	107	2	US-08-468-819-5	Sequence 5, Appl
59	7	2.4	107	3	US-09-203-235-7	Sequence 7, Appl
60	7	2.4	107	4	US-09-213-383-5	Sequence 5, Appl
61	7	2.4	107	5	PCT-US95-16144-7	Sequence 7, Appl
62	7	2.4	145	3	US-08-808-599A-41	Sequence 41, Appl
63	7	2.4	218	4	US-09-084-303B-204	Sequence 204, App
64	7	2.4	309	1	US-08-723-202-1	Sequence 1, Appl
65	7	2.4	309	1	US-08-896-371-1	Sequence 1, Appl
66	7	2.4	331	4	US-09-830-217-18	Sequence 18, Appl
67	7	2.4	344	4	US-09-252-991A-31786	Sequence 31786, A
68	7	2.4	345	4	US-09-252-991A-17809	Sequence 17809, A
69	7	2.4	373	4	US-09-107-532A-7048	Sequence 7048, Ap
70	7	2.4	385	4	US-09-489-039A-10159	Sequence 10159, A
71	7	2.4	388	1	US-08-087-772A-2	Sequence 2, Appl
72	7	2.4	400	1	US-07-916-901-6	Sequence 6, Appl
73	7	2.4	400	1	US-07-783-602C-1	Sequence 1, Appl
74	7	2.4	400	1	US-08-351-473B-4	Sequence 4, Appl
75	7	2.4	400	1	US-08-351-473B-5	Sequence 5, Appl
76	7	2.4	400	3	US-08-450-962-4	Sequence 4, Appl
77	7	2.4	400	3	US-08-450-962-6	Sequence 6, Appl
78	7	2.4	400	4	US-08-848-631-6	Sequence 4, Appl
79	7	2.4	400	4	US-08-848-631-6	Sequence 4, Appl
80	7	2.4	422	4	US-09-679-279-17	Sequence 17, Appl
81	7	2.4	511	4	US-09-002-285-88	Sequence 88, Appl
82	7	2.4	511	4	US-09-589-477-88	Sequence 88, Appl
83	7	2.4	512	4	US-09-489-039A-7179	Sequence 7179, Ap
84	7	2.4	519	4	US-08-198-452A-97179	Sequence 97179, App
85	7	2.4	520	4	US-09-252-991A-30677	Sequence 30677, A
86	7	2.4	521	2	US-08-682-847-4	Sequence 4, Appl
87	7	2.4	562	4	US-09-674-826B-4	Sequence 53, Appl
88	7	2.4	564	1	US-07-872-644-53	Sequence 53, Appl
89	7	2.4	564	1	US-08-297-494-53	Sequence 53, Appl
90	7	2.4	564	1	US-08-297-510-53	Sequence 53, Appl
91	7	2.4	564	1	US-08-479-532-53	Sequence 53, Appl
92	7	2.4	564	1	US-08-455-526-53	Sequence 53, Appl
93	7	2.4	564	1	US-08-455-526-53	Sequence 53, Appl
94	7	2.4	564	3	US-09-139-491-53	Sequence 53, Appl
95	7	2.4	564	4	US-09-883-825-53	Sequence 53, Appl
96	7	2.4	564	5	PCT-US92-03222-53	Sequence 53, Appl
97	7	2.4	634	1	US-07-872-644-51	Sequence 51, Appl
98	7	2.4	634	1	US-08-297-494-51	Sequence 51, Appl
99	7	2.4	634	1	US-08-297-510-51	Sequence 51, Appl
100	7	2.4	634	1	US-08-479-532-51	Sequence 51, Appl

247	6	2.1	95	3	US-08-946-329A-78	Sequence 78, Appl	320	6	2.1	187	4	US-09-328-352-5718	Sequence 5718, Ap
248	6	2.1	100	4	US-09-352-991A-22568	Sequence 22568, A	321	6	2.1	191	4	US-09-489-039A-12833	Sequence 12833, A
249	6	2.1	100	4	US-09-134-000C-5929	Sequence 5929, Ap	322	6	2.1	193	4	US-09-107-532A-4855	Sequence 4855, Ap
250	6	2.1	103	2	US-08-448-561-4	Sequence 4, Appl	323	6	2.1	197	4	US-08-855-261A-1	Sequence 1, Appl
251	6	2.1	104	2	US-08-616-392C-12	Sequence 12, Appl	324	6	2.1	197	4	US-08-227-224-1	Sequence 1, Appl
252	6	2.1	110	4	US-09-149-476-593	Sequence 593, Ap	325	6	2.1	197	4	US-09-855-288-1	Sequence 1, Appl
253	6	2.1	110	4	US-09-547-435-22	Sequence 22, Appl	326	6	2.1	198	4	US-09-227-357-232	Sequence 232, Ap
254	6	2.1	112	4	US-08-858-207A-358	Sequence 358, Ap	327	6	2.1	198	4	US-09-800-170-28	Sequence 28, Appl
255	6	2.1	113	3	US-09-345-041-125	Sequence 125, Ap	328	6	2.1	199	4	US-09-800-170-28	Sequence 28, Appl
256	6	2.1	114	4	US-09-107-532A-5394	Sequence 5394, Ap	329	6	2.1	202	4	US-08-679-493A-197	Sequence 197, Ap
257	6	2.1	116	3	US-08-545-809A-92	Sequence 92, Appl	330	6	2.1	206	4	US-08-205-258-463	Sequence 463, Ap
258	6	2.1	116	3	US-08-545-809A-118	Sequence 118, Ap	331	6	2.1	206	4	US-08-107-532A-6952	Sequence 6952, Ap
259	6	2.1	116	3	US-08-545-809A-140	Sequence 140, Ap	332	6	2.1	206	4	US-09-540-236-3153	Sequence 3153, Ap
260	6	2.1	116	4	US-09-462-917A-22	Sequence 22, Appl	333	6	2.1	210	4	US-09-134-001C-4065	Sequence 4065, Ap
261	6	2.1	116	4	US-09-328-352-7417	Sequence 7417, Ap	334	6	2.1	210	4	US-09-252-991A-30886	Sequence 30886, A
262	6	2.1	117	3	US-08-545-809A-114	Sequence 114, Ap	335	6	2.1	217	4	US-08-679-493A-196	Sequence 196, Ap
263	6	2.1	117	3	US-09-489-039A-12399	Sequence 12399, A	336	6	2.1	218	3	US-09-113-750A-9	Sequence 9, Appl
264	6	2.1	118	3	US-08-545-809A-116	Sequence 116, Ap	337	6	2.1	220	1	US-08-225-989-19	Sequence 19, Appl
265	6	2.1	118	3	US-08-545-809A-123	Sequence 123, Ap	338	6	2.1	220	1	US-08-570-923-19	Sequence 19, Appl
266	6	2.1	118	3	US-08-545-809A-132	Sequence 132, Ap	339	6	2.1	220	1	US-08-580-014-19	Sequence 19, Appl
267	6	2.1	120	3	US-08-545-809A-137	Sequence 137, Ap	340	6	2.1	220	3	US-09-079-785-19	Sequence 19, Appl
268	6	2.1	121	4	US-09-352-991A-26954	Sequence 26954, A	341	6	2.1	220	4	US-09-628-126-19	Sequence 19, Appl
269	6	2.1	125	4	US-09-134-001C-5034	Sequence 5034, Ap	342	6	2.1	221	4	US-08-679-493A-198	Sequence 198, Ap
270	6	2.1	126	2	US-08-561-521-2	Sequence 2, Appl	343	6	2.1	221	4	US-08-874-926-2	Sequence 2, Appl
271	6	2.1	126	2	US-08-561-521-15	Sequence 15, Appl	344	6	2.1	222	4	US-08-384-162-8	Sequence 8, Appl
272	6	2.1	126	4	US-09-107-532A-7133	Sequence 7133, Ap	345	6	2.1	234	4	US-09-543-681A-4712	Sequence 4712, Ap
273	6	2.1	126	5	PCT-US95-01219-2	Sequence 2, Appl	346	6	2.1	236	4	US-09-252-991A-29709	Sequence 29709, A
274	6	2.1	126	5	PCT-US95-01219-15	Sequence 15, Appl	347	6	2.1	239	1	US-08-225-989-6	Sequence 6, Appl
275	6	2.1	128	1	US-08-339-582-4	Sequence 4, Appl	348	6	2.1	239	1	US-08-570-923-6	Sequence 6, Appl
276	6	2.1	130	2	US-08-944-449-2	Sequence 2, Appl	349	6	2.1	239	1	US-08-580-014-6	Sequence 6, Appl
277	6	2.1	130	4	US-09-353-362-2	Sequence 2, Appl	350	6	2.1	239	3	US-09-079-785-6	Sequence 6, Appl
278	6	2.1	130	4	US-08-489-039A-13887	Sequence 13887, A	351	6	2.1	239	4	US-09-921-667-4	Sequence 4, Appl
279	6	2.1	131	1	US-08-441-629-6	Sequence 6, Appl	352	6	2.1	239	4	US-09-628-126-6	Sequence 6, Appl
280	6	2.1	131	3	US-08-776-207-6	Sequence 6, Appl	353	6	2.1	241	4	US-09-328-352-8001	Sequence 8001, Ap
281	6	2.1	131	4	US-09-507-773-6	Sequence 6, Appl	354	6	2.1	241	4	US-09-543-681A-5245	Sequence 5245, Ap
282	6	2.1	131	5	PCT-US95-09172-6	Sequence 6, Appl	355	6	2.1	248	4	US-09-252-991A-23110	Sequence 23110, A
283	6	2.1	132	2	US-08-616-392C-10	Sequence 10, Appl	356	6	2.1	253	4	US-09-543-681A-6581	Sequence 6581, Ap
284	6	2.1	132	4	US-08-635-109-1	Sequence 1, Appl	357	6	2.1	256	4	US-08-232-412-2	Sequence 2, Appl
285	6	2.1	133	4	US-08-352-991A-29953	Sequence 29953, A	358	6	2.1	257	4	US-08-205-258-293	Sequence 293, Ap
286	6	2.1	134	4	US-09-621-976-3902	Sequence 3902, Ap	359	6	2.1	257	4	US-09-489-039A-13129	Sequence 13129, A
287	6	2.1	137	1	US-09-149-476-393	Sequence 393, Ap	360	6	2.1	257	4	US-09-134-000C-6129	Sequence 6129, Ap
288	6	2.1	139	1	US-08-478-039-108	Sequence 108, Ap	361	6	2.1	258	2	US-08-847-900-4	Sequence 4, Appl
289	6	2.1	139	1	US-08-476-349A-108	Sequence 108, Ap	362	6	2.1	264	4	US-09-107-532A-4581	Sequence 4581, Ap
290	6	2.1	139	3	US-08-523-894-2	Sequence 2, Appl	363	6	2.1	264	4	US-09-489-039A-10454	Sequence 10454, A
291	6	2.1	139	4	US-09-252-991A-31236	Sequence 31236, A	364	6	2.1	270	2	US-08-773-368-1	Sequence 1, Appl
292	6	2.1	139	4	US-08-547-435-18	Sequence 18, Appl	365	6	2.1	270	3	US-09-199-887-1	Sequence 1, Appl
293	6	2.1	140	4	US-09-489-039A-10789	Sequence 10789, A	366	6	2.1	273	4	US-09-252-991A-16693	Sequence 16693, A
294	6	2.1	142	2	US-08-480-774A-2	Sequence 2, Appl	367	6	2.1	275	3	US-08-976-255-16	Sequence 16, Appl
295	6	2.1	142	3	US-08-908-643C-53	Sequence 53, Appl	368	6	2.1	275	4	US-09-107-532A-5237	Sequence 5237, Ap
296	6	2.1	142	3	US-08-847-065-21	Sequence 21, Appl	369	6	2.1	275	4	US-09-134-000C-6042	Sequence 6042, Ap
297	6	2.1	147	4	US-09-252-991A-22087	Sequence 22087, A	370	6	2.1	278	4	US-09-149-476-454	Sequence 454, Ap
298	6	2.1	148	4	US-09-621-976-3957	Sequence 3957, Ap	371	6	2.1	278	4	US-09-543-681A-5811	Sequence 5811, Ap
299	6	2.1	150	4	US-08-821-976-4059	Sequence 4059, Ap	372	6	2.1	278	4	US-09-134-000C-5311	Sequence 5311, Ap
300	6	2.1	151	2	US-08-722-050-8	Sequence 8, Appl	373	6	2.1	281	4	US-09-512-251A-9	Sequence 9, Appl
301	6	2.1	151	4	US-09-883-985-8	Sequence 8, Appl	374	6	2.1	281	4	US-09-515-150A-9	Sequence 9, Appl
302	6	2.1	153	2	US-08-791-924-1	Sequence 1, Appl	375	6	2.1	281	4	US-09-196-881-12	Sequence 12, Appl
303	6	2.1	155	4	US-09-800-170-54	Sequence 54, Appl	376	6	2.1	285	4	US-09-252-991A-23332	Sequence 23332, A
304	6	2.1	156	4	US-09-732-210-1642	Sequence 1642, Ap	377	6	2.1	286	4	US-09-543-681A-4840	Sequence 4840, Ap
305	6	2.1	157	4	US-09-340-236-3711	Sequence 3731, Ap	378	6	2.1	289	4	US-09-252-991A-23564	Sequence 23564, A
306	6	2.1	159	4	US-09-205-258-615	Sequence 615, Ap	379	6	2.1	291	4	US-09-547-435-14	Sequence 14, Appl
307	6	2.1	161	4	US-09-252-991A-22676	Sequence 22676, A	380	6	2.1	292	4	US-09-651-200-16	Sequence 16, Appl
308	6	2.1	161	4	US-09-252-991A-28429	Sequence 28429, A	381	6	2.1	292	4	US-09-303-040-2	Sequence 2, Appl
309	6	2.1	162	4	US-09-252-991A-24953	Sequence 24953, A	382	6	2.1	292	4	US-09-303-040-4	Sequence 4, Appl
310	6	2.1	166	3	US-08-908-643C-51	Sequence 51, Appl	383	6	2.1	292	4	US-09-543-681A-5561	Sequence 5561, Ap
311	6	2.1	166	4	US-09-134-001C-5417	Sequence 5417, Ap	384	6	2.1	293	4	US-09-252-991A-31017	Sequence 31017, A
312	6	2.1	170	4	US-08-328-352-8037	Sequence 8037, Ap	385	6	2.1	294	4	US-09-540-236-2814	Sequence 2814, Ap
313	6	2.1	173	4	US-09-252-991A-27863	Sequence 27863, A	386	6	2.1	296	1	US-08-261-662-2	Sequence 2, Appl
314	6	2.1	174	2	US-08-683-262B-59	Sequence 59, Appl	387	6	2.1	296	5	PCT-US95-07752-2	Sequence 2, Appl
315	6	2.1	174	3	US-09-361-707-59	Sequence 59, Appl	388	6	2.1	300	4	US-09-794-960-5	Sequence 5, Appl
316	6	2.1	174	4	US-09-107-532A-4203	Sequence 4203, Ap	389	6	2.1	304	4	US-09-252-991A-22398	Sequence 22398, A
317	6	2.1	174	4	US-09-489-039A-12363	Sequence 12363, A	390	6	2.1	304	4	US-09-489-039A-14181	Sequence 14181, A
318	6	2.1	178	4	US-09-216-393B-137	Sequence 137, Ap	391	6	2.1	306	4	US-09-252-991A-30395	Sequence 30395, A
319	6	2.1	179	4	US-09-352-991A-23620	Sequence 23620, A	392	6	2.1	311	1	US-08-118-270-37	Sequence 37, Appl

393	6	2.1	311	5	PCT-US93-08528-37	Sequence 37, Appl	466	6	2.1	427	4	US-08-311-731A-216	Sequence 216, Appl
394	6	2.1	312	4	US-09-252-991A-23610	Sequence 23610, A	467	6	2.1	429	4	US-09-372-425A-6	Sequence 6, Appl
395	6	2.1	317	4	US-08-543-681A-4278	Sequence 4278, Ap	468	6	2.1	429	4	US-09-328-352-4643	Sequence 4643, Ap
396	6	2.1	318	4	US-09-759-281B-1	Sequence 1, Appl	469	6	2.1	431	4	US-09-800-170-1	Sequence 1, Appl
397	6	2.1	319	4	US-09-358-383C-22	Sequence 22, Appl	470	6	2.1	431	4	US-08-543-681A-6326	Sequence 6326, Ap
398	6	2.1	321	4	US-09-582-660-5	Sequence 5, Appl	471	6	2.1	431	4	US-08-543-681A-7623	Sequence 7623, Ap
399	6	2.1	324	4	US-09-489-039A-12945	Sequence 12945, A	472	6	2.1	433	4	US-08-252-991A-25248	Sequence 25248, A
400	6	2.1	327	4	US-08-748-068-2	Sequence 2, Appl	473	6	2.1	433	4	US-09-328-352-6503	Sequence 6503, Ap
401	6	2.1	330	4	US-09-252-991A-24853	Sequence 24853, A	474	6	2.1	434	4	US-09-800-170-48	Sequence 48, Appl
402	6	2.1	333	4	US-09-107-532A-4698	Sequence 4698, Ap	475	6	2.1	435	3	US-08-911-321-8	Sequence 8, Appl
403	6	2.1	334	4	US-09-252-991A-20310	Sequence 20310, A	476	6	2.1	437	4	US-09-800-170-49	Sequence 49, Appl
404	6	2.1	334	4	US-09-489-039A-9328	Sequence 9328, Ap	477	6	2.1	438	4	US-09-800-170-30	Sequence 30, Appl
405	6	2.1	338	4	US-08-218-686-2	Sequence 2, Appl	477	6	2.1	438	4	US-09-800-170-32	Sequence 32, Appl
406	6	2.1	338	4	US-08-460-242-2	Sequence 60, Appl	479	6	2.1	438	4	US-09-800-170-34	Sequence 34, Appl
407	6	2.1	338	4	US-09-325-932A-60	Sequence 3258, Ap	480	6	2.1	438	4	US-09-800-170-36	Sequence 36, Appl
408	6	2.1	342	4	US-09-134-001C-3258	Sequence 3258, Ap	481	6	2.1	438	4	US-09-800-170-38	Sequence 38, Appl
409	6	2.1	342	4	US-09-489-039A-8662	Sequence 8662, Ap	482	6	2.1	438	4	US-09-800-170-40	Sequence 40, Appl
410	6	2.1	355	4	US-09-252-991A-18900	Sequence 18900, A	483	6	2.1	438	4	US-09-800-170-42	Sequence 42, Appl
411	6	2.1	359	4	US-09-134-001C-4842	Sequence 4842, Ap	484	6	2.1	438	4	US-09-800-170-44	Sequence 44, Appl
412	6	2.1	359	4	US-09-266-565-120	Sequence 120, App	485	6	2.1	438	4	US-09-800-170-46	Sequence 46, Appl
413	6	2.1	360	4	US-09-252-991A-17420	Sequence 17420, A	486	6	2.1	438	4	US-08-489-039A-8527	Sequence 8527, Ap
414	6	2.1	362	4	US-09-134-001C-5403	Sequence 5403, Ap	487	6	2.1	441	4	US-09-543-681A-7207	Sequence 7207, Ap
415	6	2.1	365	4	US-09-328-352-6517	Sequence 6517, Ap	488	6	2.1	441	4	US-09-610-006-1	Sequence 4669, Ap
416	6	2.1	369	4	US-09-489-039A-7587	Sequence 7587, Ap	489	6	2.1	444	4	US-09-489-039A-10922	Sequence 10922, A
417	6	2.1	375	4	US-09-489-039A-9807	Sequence 9807, Ap	490	6	2.1	444	4	US-08-660-451A-12	Sequence 12, Appl
418	6	2.1	376	2	US-08-933-750C-25	Sequence 25, Appl	491	6	2.1	446	4	US-09-107-532A-5776	Sequence 5776, Ap
419	6	2.1	376	3	US-09-234-613-25	Sequence 25, Appl	492	6	2.1	446	4	US-08-372-425A-2	Sequence 2, Appl
420	6	2.1	376	4	US-09-252-991A-21512	Sequence 21512, A	493	6	2.1	447	4	US-08-252-991A-17422	Sequence 17422, A
421	6	2.1	376	4	US-09-252-991A-23396	Sequence 23396, A	494	6	2.1	447	4	US-09-071-434-1	Sequence 1, Appl
422	6	2.1	378	4	US-09-325-932A-158	Sequence 158, Ap	495	6	2.1	450	3	US-09-413-814-101	Sequence 101, App
423	6	2.1	383	1	US-08-230-448A-78	Sequence 78, Appl	496	6	2.1	454	3	US-09-109-204-1	Sequence 1, Appl
424	6	2.1	383	1	US-08-230-448A-78	Sequence 78, Appl	497	6	2.1	454	3	US-09-490-032-1	Sequence 1, Appl
425	6	2.1	383	1	US-08-175-069A-78	Sequence 78, Appl	498	6	2.1	457	2	US-08-847-900-3	Sequence 3, Appl
426	6	2.1	383	4	US-08-461-939B-78	Sequence 78, Appl	499	6	2.1	457	2	US-08-847-900-3	Sequence 3, Appl
427	6	2.1	384	4	US-08-464-000-78	Sequence 78, Appl	500	6	2.1	458	2	US-08-655-878-2	Sequence 2, Appl
428	6	2.1	384	4	US-09-489-039A-13733	Sequence 13733, A	501	6	2.1	458	4	US-09-489-039A-13954	Sequence 13954, A
429	6	2.1	385	4	US-09-820-005-2	Sequence 2, Appl	502	6	2.1	462	4	US-09-328-352-6888	Sequence 6888, Ap
430	6	2.1	388	4	US-09-215-405-24	Sequence 24, Appl	503	6	2.1	462	4	US-09-907-794A-285	Sequence 285, App
431	6	2.1	390	4	US-08-800-005-4	Sequence 4, Appl	504	6	2.1	463	4	US-09-905-135A-285	Sequence 285, App
432	6	2.1	393	3	US-08-888-429A-21	Sequence 21, Appl	505	6	2.1	463	4	US-09-902-775A-285	Sequence 285, App
433	6	2.1	393	4	US-09-533-653-21	Sequence 21, Appl	506	6	2.1	465	4	US-09-292-097-15	Sequence 15, Appl
434	6	2.1	397	4	US-09-252-991A-20668	Sequence 20668, A	507	6	2.1	466	4	US-09-252-991A-26545	Sequence 26545, A
435	6	2.1	401	3	US-08-517-802-3	Sequence 3, Appl	508	6	2.1	467	3	US-08-523-894-8	Sequence 8, Appl
436	6	2.1	401	4	US-09-252-991A-17272	Sequence 17272, A	509	6	2.1	467	3	US-08-523-894-10	Sequence 10, Appl
437	6	2.1	402	4	US-09-252-991A-26529	Sequence 26529, A	510	6	2.1	467	3	US-08-523-894-12	Sequence 12, Appl
438	6	2.1	403	4	US-09-489-039A-11877	Sequence 11877, A	511	6	2.1	469	4	US-09-332-041-3	Sequence 3, Appl
439	6	2.1	408	4	US-09-252-991A-25757	Sequence 25757, A	512	6	2.1	469	4	US-09-489-039A-14044	Sequence 14044, A
440	6	2.1	411	1	US-08-399-561-2	Sequence 2, Appl	513	6	2.1	471	4	US-09-252-991A-18975	Sequence 18975, A
441	6	2.1	415	4	US-09-252-991A-26760	Sequence 26760, A	514	6	2.1	471	4	US-09-489-039A-12418	Sequence 12418, A
442	6	2.1	416	4	US-09-328-352-4168	Sequence 4168, Ap	515	6	2.1	473	3	US-09-049-672A-4	Sequence 4, Appl
443	6	2.1	421	2	US-08-576-326A-53	Sequence 53, Appl	516	6	2.1	473	4	US-09-134-001C-3564	Sequence 3564, Ap
444	6	2.1	422	4	US-08-634-238-226	Sequence 226, App	517	6	2.1	474	4	US-09-489-039A-13282	Sequence 13282, A
445	6	2.1	425	1	US-07-657-769B-69	Sequence 69, Appl	518	6	2.1	475	4	US-09-252-991A-30242	Sequence 30242, A
446	6	2.1	425	1	US-08-097-938-7	Sequence 7, Appl	519	6	2.1	476	3	US-08-487-550-4	Sequence 4, Appl
447	6	2.1	425	1	US-08-097-938-7	Sequence 7, Appl	520	6	2.1	476	3	US-08-487-550-4	Sequence 4, Appl
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Sequence 11, Appli	
Sequence 10, Appli	
Sequence 609, App	
Sequence 10, Appli	
Sequence 138, App	
Sequence 23, Appli	
Sequence 3, Appli	
Sequence 10, Appli	
Sequence 11, Appli	
Sequence 11, Appli	
Sequence 615, App	
Sequence 116, App	
Sequence 2, Appli	
Sequence 116, App	
Sequence 11, Appli	
Sequence 23, Appli	
Sequence 6, Appli	
Sequence 23, Appli	
Sequence 95, Appli	
Sequence 94, Appli	
Sequence 23, Appli	
Sequence 4, Appli	
Sequence 23, Appli	


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977      5      1.7      18      1      US-08-295-085-7      Sequence 7, Appli
978      5      1.7      18      1      US-08-295-085-8      Sequence 8, Appli
979      5      1.7      18      1      US-08-709-915-4      Sequence 4, Appli
980      5      1.7      18      2      US-08-746-283-19      Sequence 19, Appli
981      5      1.7      18      2      US-08-569-188-5      Sequence 5, Appli
982      5      1.7      18      2      US-08-569-188-6      Sequence 6, Appli
983      5      1.7      18      2      US-08-569-188-15      Sequence 15, Appli
984      5      1.7      18      2      US-08-569-188-17      Sequence 17, Appli
985      5      1.7      18      3      US-08-746-257A-17      Sequence 17, Appli
986      5      1.7      18      3      US-08-779-764A-40      Sequence 40, Appli
987      5      1.7      18      3      US-09-101-146-42      Sequence 42, Appli
988      5      1.7      18      3      US-09-248-588-91      Sequence 91, Appli
989      5      1.7      18      4      US-09-450-315A-1      Sequence 1, Appli
990      5      1.7      18      4      US-09-447-966-1      Sequence 1, Appli
991      5      1.7      18      4      US-09-563-456-40      Sequence 40, Appli
992      5      1.7      18      4      US-09-428-082B-179      Sequence 179, App
993      5      1.7      18      4      US-10-083-889-15      Sequence 15, Appli
994      5      1.7      18      5      PCT-US94-07019-5      Sequence 5, Appli
995      5      1.7      18      5      PCT-US94-07019-6      Sequence 6, Appli
996      5      1.7      18      5      PCT-US94-07019-15      Sequence 15, Appli
997      5      1.7      18      5      PCT-US95-10741-3      Sequence 3, Appli
998      5      1.7      18      5      PCT-US95-10741-4      Sequence 4, Appli
999      5      1.7      18      5      PCT-US95-10741-5      Sequence 5, Appli
1000     5      1.7      18      5      PCT-US95-10741-6      Sequence 6, Appli
          5      1.7      18      5      PCT-US95-10741-7      Sequence 7, Appli

```

ALIGNMENTS

```

RESULT 1
US-08-955-937A-4
; Sequence 4, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-955-937A-4
Query Match      3.4%; Score 10; DB 3; Length 195;
Best Local Similarity 100.0%; Pred.No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78      DRVSIKDNQK 87
      |||||
DB      74      DRVSIKDNQK 83
      |||||

RESULT 2
US-09-300-985-4
; Sequence 4, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (122) (170) (184)
US-09-300-985-4
Query Match      3.4%; Score 10; DB 3; Length 195;
Best Local Similarity 100.0%; Pred.No. 0.08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      78      DRVSIKDNQK 87
      |||||
DB      74      DRVSIKDNQK 83
      |||||

RESULT 3
US-08-955-937A-2
; Sequence 2, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 201 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-937A-2

Query Match          3.4%; Score 10; DB 3; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DRVSIXDNQK 87
DB 74 DRVSIXDNQK 83

RESULT 4
US-09-300-985-2
; Sequence 2, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HUBLE, MARK ROBERT
; TITLE OF INVENTION: FIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 201
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-300-985-2

Query Match          3.4%; Score 10; DB 3; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DRVSIXDNQK 87
DB 74 DRVSIXDNQK 83

RESULT 5
US-08-352-324A-4
; Sequence 4, Application US/08352324A
; Patent No. 5633149
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,324A
; FILING DATE: 07-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0025 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-352-324A-4

Query Match          2.8%; Score 8; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVVAAS 174
DB 22 LLLVVAAS 29

RESULT 6
US-08-862-607-4
; Sequence 4, Application US/08862607
; Patent No. 5844084
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/862,607
FILING DATE: 23-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0195
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-862-607-4

Query Match 2.8%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 7
US-08-468-819-6
Sequence 6, Application US/08468819
Patent No. 5971723
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
APPLICANT: Polverini, Peter J.
APPLICANT: Kunkel, Steven L.
TITLE OF INVENTION: CXK Chemokines as Regulators of
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,819
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC-003/HVL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-468-819-6

Query Match 2.8%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 8
US-09-203-235-4
Sequence 4, Application US/09203235
Patent No. 6071701
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
INFLAMED ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/203,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,607
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-203-235-4

Query Match 2.8%; Score 8; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 9
US-09-213-383-6
Sequence 6, Application US/09213383
Patent No. 6491906

```
;;
;; GENERAL INFORMATION:
;; APPLICANT: Strieter, Robert M.
;; Polverini, Peter J.
;; Kunkel, Steven L.
;; TITLE OF INVENTION: CXC Chemokines as Regulators of
;; Angiogenesis
;; NUMBER OF SEQUENCES: 93
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: US
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/213,383
;; FILING DATE: 09-Dec-1998
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/468,819
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Highlander, Steven L.
;; REGISTRATION NUMBER: 37,642
;; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7477
;; TELEX: N/A
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-213-383-6
Query Match 2.8%; Score 8; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 10
PCT-US95-16144-4
; Sequence 4, Application PC/TUS9516144
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFLAMED
; TISSUE OF INVENTION: ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1/MS-DOS 6.2
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;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/16144
;; FILING DATE: 07-DEC-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/352,324
;; FILING DATE: 07-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LUTHER, BARBARA J.
;; REGISTRATION NUMBER: 33954
;; REFERENCE/DOCKET NUMBER: PF-0025 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-852-0195
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US95-16144-4
Query Match 2.8%; Score 8; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVVAAS 174
Db 22 LLLVVAAS 29

RESULT 11
US-09-582-934-2
; Sequence 2, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: we really
; OTHER INFORMATION: don't know.
US-09-582-934-2
Query Match 2.8%; Score 8; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 ASLLAWRM 180
Db 195 ASLLAWRM 202

RESULT 12
US-09-582-934-1
; Sequence 1, Application US/09582934
; Patent No. 6617428
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N.J.
; TITLE OF INVENTION: Human CMRF-35-H9 receptor which binds IGM
```

```

; FILE REFERENCE: HART
; CURRENT APPLICATION NUMBER: US/09/582,934
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 329582
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00003
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:we really don't
; OTHER INFORMATION: know
US-09-582-934-1

Query Match      2.8%; Score 8; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 ASLLAWRM 180
Db 195 ASLLAWRM 202

RESULT 13
US-09-348-578-4
; Sequence 4, Application US/09348578
; Patent No. 6160089
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/348,578
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 193003/1998
; EARLIER FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA secretion
; OTHER INFORMATION: signal
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-09-348-578-4

Query Match      2.4%; Score 7; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLLVAA 173
Db 9 LLLLVAA 15

RESULT 14
US-09-699-684-4
; Sequence 4, Application US/09699684
; Patent No. 6436674
; GENERAL INFORMATION:
; APPLICANT: HONJO, Masaru
; APPLICANT: NAITOH, Naokazu
; APPLICANT: UCHIDA, Hiroshi
; APPLICANT: MOCHIZUKI, Daisuke
; APPLICANT: MATSUMOTO, Kazuya
; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE
; FILE REFERENCE: 029430-421
; CURRENT APPLICATION NUMBER: US/09/699,684
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/348,578
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence:Modified OppA secretion
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US-09-699-684-4

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RESULT 15
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; Sequence 9, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-087-772A-9

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Query Match 2.4%; Score 7; DB 1; Length 30;
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QY 275 GRCPEEP 281
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OM protein - protein search, using sw model

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721.928 Million cell updates/sec

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742	7	2.4	233	12	US-10-424-599-195297	Sequence 195297,	815	7	2.4	579	10	US-09-890-688-72	Sequence 72, Appl
743	7	2.4	235	10	US-09-834-597-349	Sequence 349, App	816	7	2.4	582	12	US-10-424-599-251471	Sequence 251471, A
744	7	2.4	235	15	US-10-277-216-349	Sequence 349, App	817	7	2.4	599	15	US-10-369-493-17309	Sequence 17309, A
745	7	2.4	235	16	US-10-126-022-349	Sequence 349, App	818	7	2.4	614	12	US-10-335-977-5287	Sequence 5287, Ap


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965 7 2.4 813 14 US-10-176-756-466
966 7 2.4 813 14 US-10-176-911-466
967 7 2.4 813 14 US-10-176-913-466
968 7 2.4 813 14 US-10-176-923-466
969 7 2.4 813 14 US-10-176-978-466
970 7 2.4 813 14 US-10-179-510-466
971 7 2.4 813 14 US-10-180-543-466
972 7 2.4 813 14 US-10-180-544-466
973 7 2.4 813 14 US-10-180-546-466
974 7 2.4 813 14 US-10-180-547-466
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976 7 2.4 813 14 US-10-180-555-466
977 7 2.4 813 14 US-10-180-559-466
978 7 2.4 813 14 US-10-181-000-466
979 7 2.4 813 14 US-10-183-010-466
980 7 2.4 813 14 US-10-183-012-466
981 7 2.4 813 14 US-10-184-614-466
982 7 2.4 813 14 US-10-184-623-466
983 7 2.4 813 14 US-10-184-635-466
984 7 2.4 813 14 US-10-184-637-466
985 7 2.4 813 14 US-10-184-646-466
986 7 2.4 813 14 US-10-184-647-466
987 7 2.4 813 14 US-10-184-652-466
988 7 2.4 813 14 US-10-187-594-466
989 7 2.4 813 14 US-10-187-596-466
990 7 2.4 813 14 US-10-187-745-466
991 7 2.4 813 14 US-10-187-885-466
992 7 2.4 813 14 US-10-187-886-466
993 7 2.4 813 14 US-10-199-464-466
994 7 2.4 813 14 US-10-196-756-466
995 7 2.4 813 14 US-10-176-751-466
996 7 2.4 813 14 US-10-176-760-466
997 7 2.4 813 14 US-10-176-990-466
998 7 2.4 813 14 US-10-180-541-466
999 7 2.4 813 14 US-10-180-542-466
1000 7 2.4 813 14 US-10-180-548-466

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ALIGNMENTS

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RESULT 1
US-09-965-529-18
; Sequence 18, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1562471CD1
US-09-965-529-18
Query Match 57.2%; Score 166; DB 9; Length 290;

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Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLGSYSIATQITPTTVNGLGRSLTVQCYVRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLGSYSIATQITPTTVNGLGRSLTVQCYVRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDKQKRTFTVWMDLTKDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDKQKRTFTVWMDLTKDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTDPAPVTQETSSPTLTGHHLNHRHKLKLSVLLPLIFTXILLVVAASLLAWRM 180
Db 121 VQVTTDPAPVTQETSSPTLTGHHLNHRHKLKLSVLLPLIFTXILLVVAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLPLEGDLGVADLTQLAGTSRKTATKLSAQVDQVEVEYVTMA 240
Db 181 MKYQOKAAGMSPEQVLPLEGDLGVADLTQLAGTSRKTATKLSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTVCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTVCNMG 267
RESULT 2
US-09-969-680A-18
; Sequence 18, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 1562471CD1
US-09-969-680A-18
Query Match 57.2%; Score 166; DB 10; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLGSYSIATQITPTTVNGLGRSLTVQCYVRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLGSYSIATQITPTTVNGLGRSLTVQCYVRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDKQKRTFTVWMDLTKDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDKQKRTFTVWMDLTKDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTDPAPVTQETSSPTLTGHHLNHRHKLKLSVLLPLIFTXILLVVAASLLAWRM 180
Db 121 VQVTTDPAPVTQETSSPTLTGHHLNHRHKLKLSVLLPLIFTXILLVVAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLPLEGDLGVADLTQLAGTSRKTATKLSAQVDQVEVEYVTMA 240

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Db 181 MKYQKAGMSPEQVLQPLEGDLCLYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQDEPTCYNMG 267
Db 241 SLPKEDISYASLTGAEDEQDEPTCYNMG 267

RESULT 3
US-10-219-535-40
; Sequence 40, Application US/10219535
; Publication No. US20040044179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P530F1C60
; CURRENT APPLICATION NUMBER: US/10/219,535
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-535-40

Query Match 57.2%; Score 166; DB 12; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEQVKRDRVSIKQKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQVKRDRVSIKQKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120

QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180

QY 181 MKYQKAGMSPEQVLQPLEGDLCLYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240

Db 181 MKYQKAGMSPEQVLQPLEGDLCLYADLTQLAGTSRPRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQDEPTCYNMG 267
Db 241 SLPKEDISYASLTGAEDEQDEPTCYNMG 267

RESULT 4
US-10-232-230-40
; Sequence 40, Application US/10232230
; Publication No. US20040044180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330PIC103
; CURRENT APPLICATION NUMBER: US/10/232,230
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-230-40

Query Match 57.2%; Score 166; DB 12; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60

QY 61 DCKILVKTSGSEQVKRDRVSIKQKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120
Db 61 DCKILVKTSGSEQVKRDRVSIKQKQNRFTVTVMEDLMKTDADTYWCGIEKTGNDLGVT 120

QY 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTQETSSPTLTGHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180

181	QY	KKYQOKAAGNSPEQVQLP	LEGDLICADLTILQ	LQAGTSPRKATTKLSSA	QVDOVEVEVYVNA	240
181	DB	KKYQOKAAGNSPEQVQLP	LEGDLICADLTILQ	LQAGTSPRKATTKLSSA	QVDOVEVEVYVNA	240
241	QY	SLPKEDISYASLTILGAEDQ	EPTYCNG	267		
241	DB	SLPKEDISYASLTILGAEDQ	EPTYCNG	267		

RESULT 5

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US-10-232-224-40
; Sequence 40, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1c11
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-40

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RESULT 5
US-10-227-884-40
; Sequence 40, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC279
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24

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1 PRIOR APPLICATION NUMBER: 60/090557
2 PRIOR FILING DATE: 1998-06-24
3 PRIOR APPLICATION NUMBER: 60/090691
4 PRIOR FILING DATE: 1998-06-25
5 PRIOR APPLICATION NUMBER: 60/090695
6 PRIOR FILING DATE: 1998-06-25
7 PRIOR APPLICATION NUMBER: 60/091982
8 PRIOR FILING DATE: 1998-07-07
9 PRIOR APPLICATION NUMBER: 60/095302
10 PRIOR FILING DATE: 1998-08-04
11 PRIOR APPLICATION NUMBER: 60/095318
12 PRIOR FILING DATE: 1998-08-04
13 PRIOR APPLICATION NUMBER: 60/095916
14 PRIOR FILING DATE: 1998-08-10
15 PRIOR APPLICATION NUMBER: 60/096146
16 PRIOR FILING DATE: 1998-08-11
17 PRIOR APPLICATION NUMBER: 60/096791
18 PRIOR FILING DATE: 1998-08-17
19 PRIOR APPLICATION NUMBER: 60/097986
20 PRIOR FILING DATE: 1998-08-26
21 PRIOR APPLICATION NUMBER: 60/098544
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23 PRIOR APPLICATION NUMBER: 60/099596
24 PRIOR FILING DATE: 1998-09-09
25 PRIOR APPLICATION NUMBER: 60/099598
26 PRIOR FILING DATE: 1998-09-09
27 PRIOR APPLICATION NUMBER: 60/099803
28 PRIOR FILING DATE: 1998-09-10
29 PRIOR APPLICATION NUMBER: 60/099811
30 PRIOR FILING DATE: 1998-09-10
31 PRIOR APPLICATION NUMBER: 60/099812
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33 PRIOR APPLICATION NUMBER: 60/099816
34 PRIOR FILING DATE: 1998-09-10
35 PRIOR APPLICATION NUMBER: 60/100038
36 PRIOR FILING DATE: 1998-09-11
37 PRIOR APPLICATION NUMBER: 60/100385
38 PRIOR FILING DATE: 1998-09-15
39 PRIOR APPLICATION NUMBER: 60/100390
40 PRIOR FILING DATE: 1998-09-15
41 PRIOR APPLICATION NUMBER: 60/100627
42 PRIOR FILING DATE: 1998-09-16
43 PRIOR APPLICATION NUMBER: 60/100848
44 PRIOR FILING DATE: 1998-09-18
45 PRIOR APPLICATION NUMBER: 60/100919
46 PRIOR FILING DATE: 1998-09-17
47 PRIOR APPLICATION NUMBER: 60/101477
48 PRIOR FILING DATE: 1998-09-23
49 PRIOR APPLICATION NUMBER: 60/101738
50 PRIOR FILING DATE: 1998-09-24
51 PRIOR APPLICATION NUMBER: 60/101741
52 PRIOR FILING DATE: 1998-09-24
53 PRIOR APPLICATION NUMBER: 60/101786
54 PRIOR FILING DATE: 1998-09-25
55 PRIOR APPLICATION NUMBER: 60/101916
56 PRIOR FILING DATE: 1998-09-24
57 PRIOR APPLICATION NUMBER: 60/101922
58 PRIOR FILING DATE: 1998-09-24
59 PRIOR APPLICATION NUMBER: 60/106178
60 PRIOR FILING DATE: 1998-10-28
61 PRIOR APPLICATION NUMBER: 60/106248
62 PRIOR FILING DATE: 1998-10-29
63 PRIOR APPLICATION NUMBER: 60/106464
64 PRIOR FILING DATE: 1998-10-30
65 PRIOR APPLICATION NUMBER: 60/106905
66 PRIOR FILING DATE: 1998-11-03
67 PRIOR APPLICATION NUMBER: 60/108787
68 PRIOR FILING DATE: 1998-11-17
69 PRIOR APPLICATION NUMBER: 60/108801
70 PRIOR FILING DATE: 1998-11-17
71 PRIOR APPLICATION NUMBER: 60/108849
72 PRIOR FILING DATE: 1998-11-18
73 PRIOR APPLICATION NUMBER: 60/112422

74 PRIOR FILING DATE: 1998-12-15
75 PRIOR APPLICATION NUMBER: 60/113296
76 PRIOR FILING DATE: 1998-12-22
77 PRIOR APPLICATION NUMBER: 60/113605
78 PRIOR FILING DATE: 1998-12-23
79 PRIOR APPLICATION NUMBER: 60/113621
80 PRIOR FILING DATE: 1998-12-23
81 PRIOR APPLICATION NUMBER: 60/115558
82 PRIOR FILING DATE: 1999-01-12
83 PRIOR APPLICATION NUMBER: 60/115565
84 PRIOR FILING DATE: 1999-01-12
85 PRIOR APPLICATION NUMBER: 60/115733
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87 PRIOR APPLICATION NUMBER: 60/119549
88 PRIOR FILING DATE: 1999-02-10
89 PRIOR APPLICATION NUMBER: 60/123618
90 PRIOR FILING DATE: 1999-03-10
91 PRIOR APPLICATION NUMBER: 60/125259
92 PRIOR FILING DATE: 1999-03-19
93 PRIOR APPLICATION NUMBER: 60/125775
94 PRIOR FILING DATE: 1999-03-23
95 PRIOR APPLICATION NUMBER: 60/126773
96 PRIOR FILING DATE: 1999-03-29
97 PRIOR APPLICATION NUMBER: 60/127887
98 PRIOR FILING DATE: 1999-04-05
99 PRIOR APPLICATION NUMBER: 60/130232
100 PRIOR FILING DATE: 1999-04-21
101 PRIOR APPLICATION NUMBER: 60/131022
102 PRIOR FILING DATE: 1999-04-26
103 PRIOR APPLICATION NUMBER: 60/131270
104 PRIOR FILING DATE: 1999-04-27
105 PRIOR APPLICATION NUMBER: 60/131291
106 PRIOR FILING DATE: 1999-04-27
107 PRIOR APPLICATION NUMBER: 60/131445
108 PRIOR FILING DATE: 1999-04-28
109 PRIOR APPLICATION NUMBER: 60/134287
110 PRIOR FILING DATE: 1999-05-14
111 PRIOR APPLICATION NUMBER: 60/140650
112 PRIOR FILING DATE: 1999-06-22
113 PRIOR APPLICATION NUMBER: 60/140723
114 PRIOR FILING DATE: 1999-06-22
115 PRIOR APPLICATION NUMBER: 60/141037
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117 PRIOR APPLICATION NUMBER: 60/144758
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128 PRIOR FILING DATE: 1999-08-17
129 PRIOR APPLICATION NUMBER: 60/151733
130 PRIOR FILING DATE: 1999-08-31
131 PRIOR APPLICATION NUMBER: 60/164418
132 PRIOR FILING DATE: 1999-11-09
133 PRIOR APPLICATION NUMBER: 60/166361
134 PRIOR FILING DATE: 1999-11-16
135 PRIOR APPLICATION NUMBER: 60/169445
136 PRIOR FILING DATE: 1999-12-07
137 PRIOR APPLICATION NUMBER: 60/169495
138 PRIOR FILING DATE: 1999-12-07
139 PRIOR APPLICATION NUMBER: 60/169835

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLXLLFWLSGYSIATQITGTTVNGLSLTVCVYRSQWETYLKWWCEGAIWR 60
|||||

Db 1 MPLLTYLLFWLSCYSIATQITGPTTVNGLRGLSLTVQCVYRSGWETYLKWWCRGAIR 60
QY 61 DCKILVKTSGSEOFVKRDRVSIKONQKRTFTVTMEDLMKTDADTYWCGIEKTKNDLGVT 120
Db 61 DCKILVKTSGSEOFVKRDRVSIKONQKRTFTVTMEDLMKTDADTYWCGIEKTKNDLGVT 120
QY 121 VQVTTIDPAPVQTESSPTTIGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVQTESSPTTIGHLDNRHKLKLSVLLPLIFTIXLLLVAAASLLAWRM 180
QY 181 MKYQKAAGMPEQVQLPQLEGDLVADLTQLAGTSRPRKATTKLSSAQVQDVEVEYVTMA 240
Db 181 MKYQKAAGMPEQVQLPQLEGDLVADLTQLAGTSRPRKATTKLSSAQVQDVEVEYVTMA 240
QY 241 SLPKEDISYASLTIGAEDQETFCYCNMG 267
Db 241 SLPKEDISYASLTIGAEDQETFCYCNMG 267

RESULT 7

US-10-230-163-40
; Sequence 40, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/113,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392

; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30

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; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
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Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred.No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLLEWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTLVLLLEWLSGYSIATQITGPTTVNGLERGLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTNGLGVT 120
QY 121 VQVITDPAPVTOEBTSSSPITLGHLDNRHKLKLVLLPIFTIXLLLVAAISLLAWRM 180
DB 121 VQVITDPAPVTOEBTSSSPITLGHLDNRHKLKLVLLPIFTIXLLLVAAISLLAWRM 180
QY 181 MKYQKAAAGMSPEQVLQPLEGLDLCVADITLQAGTSRPRKATTKLSSAQVQDQVEVEYVTMA 240
DB 181 MKYQKAAAGMSPEQVLQPLEGLDLCVADITLQAGTSRPRKATTKLSSAQVQDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTIGAEDEQETTCNMG 267
DB 241 SLPKEDISYASLTIGAEDEQETTCNMG 267

RESULT 8
US-10-230-338-40
; Sequence 40, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
DB 121 VQVITDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQKQAGMSPEQVLPLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQKQAGMSPEQVLPLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTYCNMG 267
DB 241 SLPKEDISYASLTGAEDEQPTYCNMG 267

RESULT 9
US-10-218-631-40
; Sequence 40, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40

; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTLYLLFWLSGYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQEVKRDVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVITDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
DB 121 VQVITDPAPVTQETSSPTLTGHHLNDRHKLKLSVLLPLIFTIXLLLLVAASLLAWRM 180
QY 181 MKYQKQAGMSPEQVLPLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQKQAGMSPEQVLPLEGDLGVADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
QY 241 SLPKEDISYASLTGAEDEQPTYCNMG 267
DB 241 SLPKEDISYASLTGAEDEQPTYCNMG 267

RESULT 10
US-10-230-414-40
; Sequence 40, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTIDPAPVTOBETSSPPLTGHHLDNRHKLKLSVLLPLFIITXILLVVAASLLAWRM 180
Db 121 VQVTIDPAPVTOBETSSPPLTGHHLDNRHKLKLSVLLPLFIITXILLVVAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLOPLEGDLQCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
Db 181 MKYQQAAGMSPQVLOPLEGDLQCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
QY 241 SLPKEDISYASLTGAEDEQPTTCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTTCNMG 267

RESULT 11
US-10-216-159A-40
; Sequence 40, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTIDPAPVTOBETSSPPLTGHHLDNRHKLKLSVLLPLFIITXILLVVAASLLAWRM 180
Db 121 VQVTIDPAPVTOBETSSPPLTGHHLDNRHKLKLSVLLPLFIITXILLVVAASLLAWRM 180
QY 181 MKYQQAAGMSPQVLOPLEGDLQCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
Db 181 MKYQQAAGMSPQVLOPLEGDLQCYADLTQLAGTSPRKATTKLSSAQVDQVEVEYVTWA 240
QY 241 SLPKEDISYASLTGAEDEQPTTCNMG 267
Db 241 SLPKEDISYASLTGAEDEQPTTCNMG 267

RESULT 12
US-10-218-849-40
; Sequence 40, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLRSLTVQCVYRSQWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQEVKRDVSIKDNQKNRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
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OY 121 VQVTDPAVTOEETSSFTLTGHHLNDRHKLKLSVLLPLFTIXLILLVAASLLAWRM 180
DB 121 VQVTDPAVTOEETSSFTLTGHHLNDRHKLKLSVLLPLFTIXLILLVAASLLAWRM 180
OY 181 MKYQKAGMSPEQVQLEGLDLCYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
DB 181 MKYQKAGMSPEQVQLEGLDLCYADLTLOLAGTSRKATTKLSSAQVDQVEVEYVTMA 240
OY 241 SLPKEDISYASLITLGAEDQETTCNMG 267
DB 241 SLPKEDISYASLITLGAEDQETTCNMG 267

RESULT 13

US-10-227-873-40
; Sequence 40, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905

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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
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; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17

;; PRIOR APPLICATION NUMBER: 60/108849
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;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
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;; PRIOR FILING DATE: 1999-11-16
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;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLYLLFWLSGYSIATQITGPTTVNGSLRGSLTVQCVYRSGMETYLKMWCRGAIWR 60
DB 1 MPLLTLYLLFWLSGYSIATQITGPTTVNGSLRGSLTVQCVYRSGMETYLKMWCRGAIWR 60
QY 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
DB 61 DCKILVKTSGSEQEVKDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGVT 120
QY 121 VQVITIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXILLVAASLLAWRM 180
DB 121 VQVITIDPAPVTOEETSSPTLTGHLDNRHKLKLSVLLPLIFTIXILLVAASLLAWRM 180
QY 181 MKYQCKAAGMSPEQVLOPLEGDLICYADITLQLAGTSRPAKATTKLSSAQVQVEVEYVTMA 240
DB 181 MKYQCKAAGMSPEQVLOPLEGDLICYADITLQLAGTSRPAKATTKLSSAQVQVEVEYVTMA 240
QY 241 SLPKEDISYASLTILGAEDQEBTYCNMG 267
DB 241 SLPKEDISYASLTILGAEDQEBTYCNMG 267
RESULT 14
US-10-227-883-40
; Sequence 40, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530FIC78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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PRIOR FILING DATE: 1999-06-22
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PRIOR FILING DATE: 1999-08-17
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; PRIOR APPLICATION NUMBER: 60/169445
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVSRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQVSRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOBETSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTOBETSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLOPLEGDLQYADLTLOLAGTSRPRKATTKLSSAQVDQVEVEYV 240
Db 181 MKYQOKAAGMSPEQVLOPLEGDLQYADLTLOLAGTSRPRKATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
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RESULT 15
US-10-219-076-40
; Sequence 40, Application US/10219076
; Publication No. US20030078379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC62
; CURRENT APPLICATION NUMBER: US/10/219,076
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 40
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-076-40

Query Match      57.2%; Score 166; DB 14; Length 290;
Best Local Similarity 99.6%; Pred. No. 6.5e-151;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
Db 1 MPELLTYLLFWLSGYSIATQITGPTTVNGLGRSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVSRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
Db 61 DCKILVKTSGSEQVSRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCGIEKTGNDLGV 120
QY 121 VQVTTIDPAPVTOBETSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
Db 121 VQVTTIDPAPVTOBETSSPTLTGHHLDNRHKLKLSVLLPLFTIXLLLVAAASLLAWRM 180
QY 181 MKYQOKAAGMSPEQVLOPLEGDLQYADLTLOLAGTSRPRKATTKLSSAQVDQVEVEYV 240
Db 181 MKYQOKAAGMSPEQVLOPLEGDLQYADLTLOLAGTSRPRKATTKLSSAQVDQVEVEYV 240
QY 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
Db 241 SLPKEDISYASLTILGAEDQEPYCNMG 267
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Search completed: September 16, 2004, 13:08:32
Job time : 142 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:49:37 ; Search time 41 Seconds

(without alignments)
680.379 Million cell updates/sec

Title: US-09-997-131-65
Perfect score: 290
Sequence: 1 MPILLYLLFWLSGSIAT.....SXLPGRGPPEPTREYSTISRP 290

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR.78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.8	107	2 JH8290	GRO-gamma precursor
2	8	2.8	107	2 JH0281	macrophage inflam
3	8	2.8	475	2 AT2439	hypothetical prote
4	8	2.8	600	2 C30171	RNase L inhibitor
5	7	2.4	92	2 C30532	macrophage inflam
6	7	2.4	99	2 D90259	hypothetical prote
7	7	2.4	107	2 A28414	melanoma growth-st
8	7	2.4	109	2 I49011	gene Ubely protein
9	7	2.4	109	2 I63169	gene Ubely protein
10	7	2.4	111	2 B70401	hypothetical prote
11	7	2.4	120	2 A87594	bleomycin resistan
12	7	2.4	120	2 C81087	hypothetical prote
13	7	2.4	145	2 D82105	conserved hypothet
14	7	2.4	164	2 B44827	FMRFamide-like pep
15	7	2.4	167	2 C86241	protein T16B5.9 [i
16	7	2.4	171	2 H83233	conserved hypothet
17	7	2.4	175	2 T21297	FMRFamide-like neu
18	7	2.4	185	2 D81239	ribosome recycling
19	7	2.4	187	2 G27248	hypothetical prote
20	7	2.4	194	2 D73357	hypothetical prote
21	7	2.4	210	2 S76316	hypothetical prote
22	7	2.4	218	2 T33545	hypothetical prote
23	7	2.4	255	2 F69962	amino acid ABC tra
24	7	2.4	257	2 B75099	hypothetical prote
25	7	2.4	258	2 G89968	extracellular ante
26	7	2.4	268	1 CDFM18	chlorophyll a/b-bi
27	7	2.4	284	2 A75422	acetyl-CoA carboxy
28	7	2.4	284	2 AH3570	nickel transport s
29	7	2.4	287	2 A84041	sulfate ABC transp

30	7	2.4	289	2 S19998	hypothetical prote
31	7	2.4	299	2 F83301	conserved hypothet
32	7	2.4	309	2 H89832	hypothetical prote
33	7	2.4	311	2 A72487	hypothetical prote
34	7	2.4	319	2 G86832	hypothetical prote
35	7	2.4	324	2 B24582	H-2 class I histoc
36	7	2.4	327	2 D75196	hypothetical prote
37	7	2.4	331	2 F89771	lipoprotein (impor
38	7	2.4	334	2 A24582	MHC class I histoc
39	7	2.4	335	1 SAVLHR	large surface anti
40	7	2.4	338	2 F95880	probable thuk, reg
41	7	2.4	340	2 A45883	MHC class I histoc
42	7	2.4	357	2 G70869	probable uroporph
43	7	2.4	361	2 I37421	glutaminyl-peptid
44	7	2.4	362	2 F75379	S-adenosylmethioni
45	7	2.4	372	2 S60207	fomF protein - Str
46	7	2.4	380	2 A50107	hypothetical prote
47	7	2.4	397	2 B72211	glutamate N-acetyl
48	7	2.4	400	2 S32804	beta-3-adrenergic
49	7	2.4	400	2 A41679	beta-3-adrenergic
50	7	2.4	400	2 A53281	beta 3-adrenergic
51	7	2.4	416	2 A70393	hypothetical prote
52	7	2.4	417	2 F70681	hypothetical prote
53	7	2.4	422	2 G84059	hypothetical prote
54	7	2.4	442	2 S19712	ubiquitin-protein
55	7	2.4	461	2 T38698	nocl protein - fis
56	7	2.4	508	2 S54264	glycoprotein GC -
57	7	2.4	513	2 E83069	60K chaperonin, pr
58	7	2.4	519	2 E70201	heat shock protein
59	7	2.4	519	2 H86602	glycoprotein gIII
60	7	2.4	521	1 VGBEHB	abc transporter in
61	7	2.4	533	2 F75124	mannitol transport
62	7	2.4	533	2 AF3449	probable sensor ki
63	7	2.4	538	2 D82180	probable sensor ki
64	7	2.4	554	2 S46346	gag polyprotein -
65	7	2.4	561	1 S53447	aspartate-ammonia
66	7	2.4	561	1 AHRVNC	asparagine synthas
67	7	2.4	587	2 E85429	hypothetical prote
68	7	2.4	598	2 D69292	aldehyde ferredoxi
69	7	2.4	599	2 G83941	ABC transporter (A
70	7	2.4	641	2 JCS648	terminal protein p
71	7	2.4	642	2 D71909	ferrous iron trans
72	7	2.4	642	2 G64605	iron(II) transport
73	7	2.4	643	2 T27429	hypothetical prote
74	7	2.4	716	1 WZEEB6	77.8K DNA helicase
75	7	2.4	725	2 A41258	a-aggglutinin core
76	7	2.4	751	2 T42597	DNA helicase/prima
77	7	2.4	822	2 T33163	hypothetical prote
78	7	2.4	900	2 A95340	cation transport p
79	7	2.4	911	1 B3HU	band 3 anion trans
80	7	2.4	968	2 A37867	transcription fact
81	7	2.4	971	2 A35697	transcription fact
82	7	2.4	989	2 AE3045	ice nucleation pro
83	7	2.4	1009	2 G98240	hypothetical prote
84	7	2.4	1010	2 T36383	probable large ATP
85	7	2.4	1013	2 T46422	hypothetical prote
86	7	2.4	1047	1 OYHUBR	natruetic peptid
87	7	2.4	1065	2 S19482	hypothetical prote
88	7	2.4	1067	2 D75625	probable extracell
89	7	2.4	1089	2 E82987	hypothetical prote
90	7	2.4	1099	2 A55405	adenylate cyclase
91	7	2.4	1103	2 JC4114	Ca2+-transporting
92	7	2.4	1184	2 G70600	hypothetical prote
93	7	2.4	1242	2 T39453	probable mrna stab
94	7	2.4	1268	2 T50252	probable transcrip
95	7	2.4	1288	2 JEO363	mitogen-activated
96	7	2.4	1400	1 I38185	protein-tyrosine k
97	7	2.4	2491	1 A28372	insulin-like growt
98	7	2.4	4717	2 T41581	hypothetical coile
99	6	2.1	21	2 S03979	testosterone 15alp
100	6	2.1	36	2 B27633	Ig lambda-2 chain
101	6	2.1	36	2 S78239	ycf32 protein - Od
102	6	2.1	47	2 S42126	hypothetical prote

103	6	2.1	48	2	A30504	Ig gamma heavy chain	176	6	2.1	137	2	S31585	Ig heavy chain V r
104	6	2.1	50	2	S05487	alpha-amylase (EC	177	6	2.1	137	2	AD1179	B. subtilis trkr p
105	6	2.1	52	2	G81516	hypothetical prote	178	6	2.1	137	2	AD1536	B. subtilis trkr p
106	6	2.1	54	2	JU0155	spore protein gamm	179	6	2.1	137	2	A69127	hypothetical prote
107	6	2.1	55	2	S29146	superoxide dismuta	180	6	2.1	138	2	A62255	two-component resp
108	6	2.1	57	2	S09493	Ig heavy chain pre	181	6	2.1	139	2	A41287	Ig heavy chain pre
109	6	2.1	58	2	T13185	hypothetical prote	182	6	2.1	139	2	S31586	Ig heavy chain V r
110	6	2.1	59	2	S35177	cytochrome P450 (c	183	6	2.1	139	2	S31696	Ig heavy chain V r
111	6	2.1	64	1	NRSRSL	neurotoxin V - EGY	184	6	2.1	139	2	B75307	hypothetical prote
112	6	2.1	64	1	NRSRSM	neurotoxin V - sco	185	6	2.1	139	2	S78052	Ig heavy chain pre
113	6	2.1	65	2	AB3394	hypothetical cytos	186	6	2.1	140	2	A49045	Ig heavy chain V r
114	6	2.1	66	2	D72607	hypothetical prote	187	6	2.1	140	2	A24770	hypothetical hybri
115	6	2.1	70	1	RGPBPK	regulatory protein	188	6	2.1	140	2	I37782	Ig variable region
116	6	2.1	76	2	T51499	hypothetical prote	189	6	2.1	140	2	H72710	hypothetical prote
117	6	2.1	77	2	A30522	Ig gamma-3 heavy c	190	6	2.1	140	2	T14936	hypothetical prote
118	6	2.1	79	2	TG6381	proteinase inhibi	191	6	2.1	141	2	T09251	embryonic abundant
119	6	2.1	79	2	B35867	conserved hypotet	192	6	2.1	142	2	H71061	hypothetical prote
120	6	2.1	79	2	AG1062	bacteriophage gene	193	6	2.1	142	2	H86046	hypothetical prote
121	6	2.1	80	2	AB1932	hypothetical prote	194	6	2.1	142	2	D91200	hypothetical prote
122	6	2.1	81	2	T31199	hypothetical prote	195	6	2.1	143	2	B41287	Ig heavy chain pre
123	6	2.1	82	2	JC7897	defensin 1 precurs	196	6	2.1	145	2	S78055	Ig heavy chain pre
124	6	2.1	84	2	TG3084	hypothetical prote	197	6	2.1	146	2	S09710	Ig heavy chain V r
125	6	2.1	86	1	RHD2S	gonadoliberin II p	198	6	2.1	147	2	S33519	Ig heavy chain V r
126	6	2.1	86	2	S72726	ip1B1 protein - My	199	6	2.1	152	2	S08350	superoxide dismuta
127	6	2.1	88	2	AG1356	hypothetical prote	200	6	2.1	152	2	S55402	hypothetical prote
128	6	2.1	90	2	G75317	hypothetical prote	201	6	2.1	153	2	S58092	hypothetical prote
129	6	2.1	91	2	C82657	hypothetical prote	202	6	2.1	154	2	H81175	hypothetical prote
130	6	2.1	92	2	S77498	ribosomal protein	203	6	2.1	155	2	S31512	Ig heavy chain - h
131	6	2.1	96	2	E90669	hypothetical prote	204	6	2.1	155	2	S31511	Ig heavy chain - h
132	6	2.1	98	2	PH1145	Ig heavy chain V r	205	6	2.1	156	2	C81868	hypothetical prote
133	6	2.1	98	2	AB2100	hypothetical prote	206	6	2.1	156	2	C64300	hypothetical prote
134	6	2.1	100	2	AB1035	probable phage tai	207	6	2.1	156	2	T29152	hypothetical prote
135	6	2.1	101	2	C83047	conserved hypotet	208	6	2.1	156	2	D81722	hypothetical prote
136	6	2.1	103	1	ZGBPS1	Gene G protein - p	209	6	2.1	156	2	AC0540	probable fibrillar
137	6	2.1	103	2	T20883	hypothetical prote	210	6	2.1	157	2	T02034	early light-induce
138	6	2.1	103	2	AS9031	ARS component B 81	211	6	2.1	159	2	T49532	large-conductance
139	6	2.1	104	2	F72753	hypothetical prote	212	6	2.1	159	2	JQ0136	hypothetical 17.8K
140	6	2.1	106	2	S56222	probable membrane	213	6	2.1	160	2	AD1061	DNA polymerase III
141	6	2.1	108	2	A13250	virA/G regulated p	214	6	2.1	160	2	C70049	flagellar protein
142	6	2.1	109	2	S12338	virH protein - Agr	215	6	2.1	162	2	F84424	probable homeodoma
143	6	2.1	109	2	H72653	hypothetical prote	216	6	2.1	163	1	YCFC3H	acetylactate synth
144	6	2.1	110	2	AB1361	Portein gp13 Bact	217	6	2.1	163	2	S15940	acetylactate synth
145	6	2.1	112	2	S24818	nifW protein Rho	218	6	2.1	163	2	F83059	acetylactate synth
146	6	2.1	113	2	S66967	probable membrane	219	6	2.1	163	2	B90639	acetylactate synth
147	6	2.1	115	2	H70778	probable acPM prot	220	6	2.1	163	2	B85490	acetylactate synth
148	6	2.1	116	2	B26340	Ig heavy chain pre	221	6	2.1	163	2	B85490	hypothetical prote
149	6	2.1	116	2	S18557	Ig heavy chain V r	222	6	2.1	164	2	D82072	hypothetical prote
150	6	2.1	116	2	G72779	hypothetical prote	223	6	2.1	164	2	AB0067	acetylactate synth
151	6	2.1	117	1	ESAD01	early E3 13K glyco	224	6	2.1	164	2	AB0517	acetylactate synth
152	6	2.1	117	2	E34964	Ig heavy chain pre	225	6	2.1	164	2	F83798	hypothetical prote
153	6	2.1	118	2	A26340	Ig heavy chain pre	226	6	2.1	165	2	AB1014	chorismate lyase I
154	6	2.1	118	2	T31776	hypothetical prote	227	6	2.1	165	2	T14781	hypothetical prote
155	6	2.1	118	2	G97857	hypothetical prote	228	6	2.1	166	2	H64605	hypothetical prote
156	6	2.1	120	2	AB1030	probable membrane	229	6	2.1	167	2	AD1978	hypothetical prote
157	6	2.1	121	2	H82473	hypothetical prote	230	6	2.1	168	2	G69217	hypothetical prote
158	6	2.1	124	1	NSHY	pancreatic ribonuc	231	6	2.1	168	2	B89836	conserved hypotet
159	6	2.1	124	2	S31684	Ig heavy chain V r	232	6	2.1	169	1	C84393	hemerthrin homolo
160	6	2.1	125	2	S09365	Ig kappa chain - m	233	6	2.1	170	2	D70621	probable argR prot
161	6	2.1	127	2	S06347	thyroglobulin - sh	234	6	2.1	171	1	OTNCV	cytochrome-c oxida
162	6	2.1	127	2	F95929	hypothetical membr	235	6	2.1	171	2	B69345	hypothetical prote
163	6	2.1	127	2	H87494	crcB protein (impo	236	6	2.1	171	2	S19502	hypothetical prote
164	6	2.1	128	2	T35073	probable phosphori	237	6	2.1	173	2	A47303	FTZ-F1 steroid rec
165	6	2.1	128	2	S73593	hypothetical prote	238	6	2.1	173	2	S19502	hypothetical prote
166	6	2.1	129	2	H83408	hypothetical prote	239	6	2.1	174	2	A70828	hypothetical prote
167	6	2.1	130	2	S22808	pancreatic ribonuc	240	6	2.1	176	2	T28764	hypothetical prote
168	6	2.1	130	2	S31673	Ig heavy chain V r	241	6	2.1	176	2	AD0472	probable fibrillar
169	6	2.1	130	2	S62401	interleukin-16 - g	242	6	2.1	178	2	AB0414	hypoxanthine phosp
170	6	2.1	132	2	JH0407	myelin P2 protein	243	6	2.1	182	2	AB2331	hypoxanthine phosp
171	6	2.1	132	2	PC4020	hypothetical 132 p	244	6	2.1	183	2	E82898	50S ribosomal prot
172	6	2.1	133	2	AG9917	hypothetical prote	245	6	2.1	184	2	S33065	conserved hypotet
173	6	2.1	134	2	G72465	hypothetical prote	246	6	2.1	185	2	A32752	type 1 fibrillar pr
174	6	2.1	135	2	S78051	Ig heavy chain pre	247	6	2.1	185	2	H50540	hypothetical prote
175	6	2.1	137	2	S31676	Ig heavy chain V r	248	6	2.1	186	2	B70595	hypothetical prote

249	6	2.1	187	2	T49222	stellacyanin (ucla	322	6	2.1	231	1	A42985	3-oxoadipate CoA-t
250	6	2.1	187	2	S22331	gene G protein - p	323	6	2.1	231	2	D81441	probable integral
251	6	2.1	187	2	JC4806	core protein G - p	324	6	2.1	231	2	C97313	uncharacterized co
252	6	2.1	187	2	A86353	hypothetical prote	325	6	2.1	232	2	G95044	conserved hypothet
253	6	2.1	187	2	R66478	protein F1504.9 [1	326	6	2.1	232	2	F97914	conserved hypothet
254	6	2.1	188	2	C90808	probable cytochrom	327	6	2.1	233	2	T36385	proline-rich prote
255	6	2.1	188	2	G95667	probable cytochrom	328	6	2.1	234	2	A81871	probable periplasm
256	6	2.1	188	2	F64848	probable membrane	329	6	2.1	235	2	F76974	hypothetical prote
257	6	2.1	188	2	G87544	exopolysaccharide	330	6	2.1	235	2	T43009	HMG protein 1.2 -
258	6	2.1	188	2	T48200	hypothetical prote	331	6	2.1	236	2	G95212	MgtC/SapB family p
259	6	2.1	191	2	E84710	hypothetical prote	332	6	2.1	236	2	G98076	Mg(2+) transport A
260	6	2.1	193	2	E75543	peptidylprolyl iso	333	6	2.1	236	2	H71056	probable arylmalon
261	6	2.1	193	2	G97238	uncharacterized me	334	6	2.1	236	2	JQ0061	hypothetical 25K p
262	6	2.1	194	2	S07260	histone H5 - musco	335	6	2.1	237	2	S55009	H+-transporting tw
263	6	2.1	195	2	F96734	probable transcrip	336	6	2.1	238	2	T35088	probable membrane
264	6	2.1	197	2	T10284	hypothetical prote	337	6	2.1	238	2	F89940	conserved hypothet
265	6	2.1	197	2	JC6544	tumor-associated a	338	6	2.1	239	2	F82386	amino acid ABC tra
266	6	2.1	197	2	F70832	probable membrane	339	6	2.1	239	2	H72667	hypothetical prote
267	6	2.1	197	2	E84606	probable WRKY-type	340	6	2.1	239	2	C72778	hypothetical prote
268	6	2.1	198	2	S73275	hypothetical prote	341	6	2.1	239	2	H75195	hypothetical prote
269	6	2.1	198	2	T08910	hypothetical prote	342	6	2.1	239	2	B40710	CD10 ligand - mous
270	6	2.1	201	2	T35017	protocatechuate 3,	343	6	2.1	240	2	JN0407	polyhedrin - Galle
271	6	2.1	201	2	T06229	probable superoxid	344	6	2.1	241	2	B64800	Glutamate/aspartat
272	6	2.1	201	2	T06800	superoxide dismuta	345	6	2.1	241	2	C90715	Glutamate/aspartat
273	6	2.1	201	2	AF2089	hypothetical prote	346	6	2.1	241	2	P85565	glutamate/aspartat
274	6	2.1	202	1	DSPMC2	superoxide dismuta	347	6	2.1	241	2	AC0583	glutamate/aspartat
275	6	2.1	203	2	A75453	conserved hypothet	348	6	2.1	242	2	A25192	C-reactive protein
276	6	2.1	203	2	AB2285	hypothetical prote	349	6	2.1	242	2	AC0131	probable copper ho
277	6	2.1	204	2	T28939	hypothetical prote	350	6	2.1	243	1	S67334	nicotinamide monon
278	6	2.1	205	2	E84334	hypothetical prote	351	6	2.1	244	1	S37397	regulatory protein
279	6	2.1	206	2	S76522	hypothetical prote	352	6	2.1	244	2	AC3341	pricornin-2 C20-me
280	6	2.1	206	2	E89961	N-acetylmuramoyl-L	353	6	2.1	244	2	A70400	hypothetical prote
281	6	2.1	207	2	E69833	conserved hypothet	354	6	2.1	245	2	C72382	conserved hypothet
282	6	2.1	208	2	S50388	hypothetical prote	355	6	2.1	245	2	T32774	hypothetical prote
283	6	2.1	209	2	G82359	conserved hypothet	356	6	2.1	246	2	S15378	H+-transporting tw
284	6	2.1	210	2	E97994	hypothetical prote	357	6	2.1	246	2	B82764	hypothetical prote
285	6	2.1	211	2	T03685	probable superoxid	358	6	2.1	247	2	T43015	hypothetical prote
286	6	2.1	211	2	E82055	sodium-type flagel	359	6	2.1	247	2	T11654	hypothetical prote
287	6	2.1	212	2	E75334	ribonuclease H1 -	360	6	2.1	247	2	A87511	conserved hypothet
288	6	2.1	212	2	B83866	hypothetical prote	361	6	2.1	248	2	JC2581	14-3-3 protein - C
289	6	2.1	212	2	AG1450	hypothetical prote	362	6	2.1	248	2	T23759	hypothetical prote
290	6	2.1	213	1	S71287	myb-related 24.7K	363	6	2.1	248	2	S76774	thiol-disulfide in
291	6	2.1	216	2	T51730	superoxide dismuta	364	6	2.1	249	2	S78186	H+-transporting tw
292	6	2.1	216	2	T38484	oligofucosyl recepto	365	6	2.1	249	2	H97161	cell division sept
293	6	2.1	217	2	S48021	superoxide dismuta	366	6	2.1	250	2	T01604	hypothetical prote
294	6	2.1	217	2	T36216	spda protein - Str	367	6	2.1	250	2	T49221	hypothetical prote
295	6	2.1	218	2	H84681	probable copper/zi	368	6	2.1	250	2	AF1095	conserved hypothet
296	6	2.1	218	2	A33136	proline/arginine-r	369	6	2.1	250	2	AI1458	conserved hypothet
297	6	2.1	218	2	T49841	hypothetical prote	370	6	2.1	251	2	AB1105	conserved hypothet
298	6	2.1	218	2	T01104	disease resistance	371	6	2.1	251	2	AB1467	hypothetical prote
299	6	2.1	220	2	H42590	M2L protein - vacc	372	6	2.1	251	2	D83855	hypothetical prote
300	6	2.1	220	2	A87552	hypothetical prote	373	6	2.1	252	2	T01947	probable membrane
301	6	2.1	221	2	AG3570	nickel transport s	374	6	2.1	252	2	S74884	hypothetical prote
302	6	2.1	222	1	DSSPC2	superoxide dismuta	375	6	2.1	252	2	F72560	hypothetical prote
303	6	2.1	223	2	S62192	probable thymidyla	376	6	2.1	252	2	A49232	outer membrane pro
304	6	2.1	224	2	T05766	peptidylprolyl iso	377	6	2.1	253	2	T22590	hypothetical prote
305	6	2.1	224	2	C48652	transfer protein s	378	6	2.1	253	2	C86325	T29M8.5 protein -
306	6	2.1	226	2	T08335	hypothetical prote	379	6	2.1	255	2	JQ2288	SPC2 protein - so
307	6	2.1	226	2	I39594	exeB protein - Aer	380	6	2.1	256	2	C89869	trans-2-enoyl-ACP
308	6	2.1	227	2	S68133	H+-transporting tw	381	6	2.1	256	2	AD2734	birA bifunctional
309	6	2.1	227	2	E69203	probable thymidyla	382	6	2.1	256	2	F97515	birA protein (AF20
310	6	2.1	228	2	T12799	conserved hypothet	383	6	2.1	256	2	T52051	probable aldehyde
311	6	2.1	228	2	B97777	hypothetical prote	384	6	2.1	258	2	F81022	probable ABC trans
312	6	2.1	229	2	F83534	arginine/ornithine	385	6	2.1	258	2	G75372	conserved hypothet
313	6	2.1	229	2	T44455	arginine/ornithine	386	6	2.1	259	2	T01008	ribonuclease (EC 3
314	6	2.1	229	2	A05198	hypothetical prote	387	6	2.1	259	2	T22862	hypothetical prote
315	6	2.1	229	2	T06346	chloroplast envelo	388	6	2.1	260	2	H93844	ABC transporter, A
316	6	2.1	229	2	F82553	hypothetical prote	389	6	2.1	260	2	H96919	hypothetical prote
317	6	2.1	230	1	G65097	hypothetical 25.5	390	6	2.1	262	2	H70953	conserved hypothet
318	6	2.1	230	2	AC2934	aspartate racemase	391	6	2.1	263	2	C81709	conserved hypothet
319	6	2.1	230	2	H91124	hypothetical prote	392	6	2.1	265	1	G69084	probable short cha
320	6	2.1	230	2	G85969	hypothetical prote	393	6	2.1	265	2	T36396	conserved hypothet
321	6	2.1	230	2	C71337	conserved hypothet	394	6	2.1	265	2	S38581	allergen Hol 1 I p

395	6	2.1	266	2	A62851	chaperone protein	468	2.1	306	2	A62042	ribosomal protein
396	6	2.1	266	2	T36287	probable integral	469	2.1	306	2	G64820	probable oligopept
397	6	2.1	266	2	H71521	probable metal dep	470	2.1	306	2	A85593	probable transport
398	6	2.1	266	2	B87994	protein Y71A12C.2	471	2.1	306	2	F90742	probable ABC t
399	6	2.1	266	2	T27362	hypothetical prote	472	2.1	306	2	AF0603	hypothetical ABC t
400	6	2.1	267	2	A30252	sugar ABC transpor	473	2.1	306	2	G83152	hypothetical prote
401	6	2.1	267	2	A32122	dolichyl-phosphate	474	2.1	307	2	T26060	hypothetical prote
402	6	2.1	267	2	B72408	conserved hypotet	475	2.1	308	2	B87059	probable pseudouri
403	6	2.1	268	2	B39429	cAMP response elem	476	2.1	308	2	A70761	hypothetical prote
404	6	2.1	268	2	B37279	enhancer-binding p	477	2.1	309	2	H95850	probable rhizopine
405	6	2.1	269	2	C91030	probable structura	478	2.1	309	2	B69956	phosphate ABC tran
406	6	2.1	269	2	A86164	protein F15K9.14 [479	2.1	309	2	B75565	hypothetical prote
407	6	2.1	269	2	D85874	probable structura	480	2.1	311	2	B95202	methionyl-tRNA for
408	6	2.1	269	2	S08346	probable structura	481	2.1	311	2	B98069	methionyl-tRNA for
409	6	2.1	269	2	AD0804	probable membrane	482	2.1	311	2	T21845	conserved hypotet
410	6	2.1	270	2	S61620	probable membrane	483	2.1	311	2	H82541	hypothetical prote
411	6	2.1	272	2	H83004	hypothetical prote	484	2.1	311	2	A97923	hypothetical prote
412	6	2.1	272	2	A81360	protein gp17 [act	485	2.1	313	2	T20812	hypothetical prote
413	6	2.1	273	2	A97488	hypothetical 30.9K	486	2.1	313	2	T18092	hypothetical prote
414	6	2.1	273	2	A42705	conserved hypotet	487	2.1	314	2	S55210	meiotic recombina
415	6	2.1	273	2	F86665	ABC transporter pe	488	2.1	314	2	E81064	cellulite resistan
416	6	2.1	273	2	D98348	hypothetical prote	489	2.1	314	2	H70723	hypothetical prote
417	6	2.1	274	2	S07999	chlorophyll a/b-bi	490	2.1	315	2	I39479	hypothetical prote
418	6	2.1	274	2	S60270	chlorophyll a/b bi	491	2.1	316	2	H95389	probable ABC trans
419	6	2.1	274	2	H70900	hypothetical prote	492	2.1	317	2	T15843	hypothetical prote
420	6	2.1	275	2	B49394	translation elonga	493	2.1	318	2	T02998	sigma-E factor reg
421	6	2.1	275	2	S76233	transcription term	494	2.1	318	2	AG0829	sigma-E factor reg
422	6	2.1	275	2	S44823	F54F2.9 protein -	495	2.1	320	2	JC1171	muscle regulatory
423	6	2.1	276	2	AF0402	transketolase [EC	496	2.1	320	2	S73124	hypothetical prote
424	6	2.1	276	2	T51685	myb-related transc	497	2.1	322	2	G87257	porphobilinogen de
425	6	2.1	279	2	H82997	conserved hypotet	498	2.1	322	2	AD0387	protein-export mem
426	6	2.1	280	2	T50554	3-methyl-2-oxobuta	499	2.1	325	2	A95958	probable periplasm
427	6	2.1	281	2	F07076	probable panB prot	500	2.1	325	2	D82662	hypothetical prote
428	6	2.1	281	2	T39464	hypothetical prote	501	2.1	326	2	A32273	MHC class I histoc
429	6	2.1	282	2	T06637	hypothetical prote	502	2.1	326	2	D83483	probable metal tra
430	6	2.1	282	2	AG1534	hypothetical prote	503	2.1	327	2	D90013	hypothetical prote
431	6	2.1	282	2	A32283	hypothetical prote	504	2.1	327	2	D82678	transcription regu
432	6	2.1	283	1	J01637	nonstructural prot	505	2.1	327	2	B36505	oxaloacetate decar
433	6	2.1	284	1	JC2526	deoxyribonuclease	506	2.1	327	2	AB0888	hypothetical prote
434	6	2.1	286	2	E87113	hypothetical prote	507	2.1	328	2	H84061	hypothetical prote
435	6	2.1	286	2	J01548	hypothetical 32.5K	508	2.1	328	2	AB1781	hypothetical prote
436	6	2.1	287	2	F82265	conserved hypotet	509	2.1	328	2	AC1405	hypothetical prote
437	6	2.1	288	2	T36224	dihydropterate sy	510	2.1	329	2	T14556	hypothetical prote
438	6	2.1	288	2	G81209	cell-binding facto	511	2.1	329	2	E90417	conserved hypotet
439	6	2.1	289	2	C87019	hypothetical prote	512	2.1	331	2	D70247	conserved hypotet
440	6	2.1	289	2	S82971	ribonuclease [EC 3	513	2.1	332	1	DEHULC	L-lactate dehydrog
441	6	2.1	289	2	B87514	metallo-beta-lacta	514	2.1	332	2	B87356	sugar ABC transpor
442	6	2.1	289	2	G83029	hypothetical prote	515	2.1	332	2	G72767	hypothetical prote
443	6	2.1	290	2	E70703	probable usPA prot	516	2.1	333	2	A41881	collagenase FtrC (
444	6	2.1	290	2	G75470	conserved hypotet	517	2.1	333	2	T19889	hypothetical prote
445	6	2.1	290	2	JC5017	calcium-modulating	518	2.1	336	2	E90014	hypothetical prote
446	6	2.1	291	2	T30267	sugar transport pr	519	2.1	336	2	C69811	nitric-oxide synth
447	6	2.1	291	2	T00855	hypothetical prote	520	2.1	336	2	T41118	hypothetical prote
448	6	2.1	291	2	C71877	hypothetical prote	521	2.1	336	2	T20854	hypothetical prote
449	6	2.1	292	2	T26879	hypothetical prote	522	2.1	336	2	AH5010	hypothetical prote
450	6	2.1	293	2	B70455	thiosulfate sulfur	523	2.1	336	2	F98273	iron(III) dicitrat
451	6	2.1	294	2	S13141	hypothetical prote	524	2.1	337	2	AG0892	probable glycoprot
452	6	2.1	294	2	F97110	permease component	525	2.1	337	2	JC5023	CMP-staic acid tr
453	6	2.1	296	2	H83480	cytochrome o ubiqu	526	2.1	337	2	AG0963	hypothetical prote
454	6	2.1	296	2	S47594	cyclophilin B-bind	527	2.1	337	2	T04035	hypothetical prote
455	6	2.1	297	2	H51332	hypothetical prote	528	2.1	338	1	TVMSEB	transforming prote
456	6	2.1	297	2	D87260	integral membrane	529	2.1	338	2	S52284	lumicon, secretory
457	6	2.1	299	2	E70842	probable acid phos	530	2.1	338	2	S06559	hypothetical prote
458	6	2.1	299	2	S54087	probable membrane	531	2.1	339	2	F96638	hypothetical prote
459	6	2.1	300	1	B71090	centrosomin homolo	532	2.1	340	2	T37030	alcohol dehydrogen
460	6	2.1	300	2	T43205	hypothetical prote	533	2.1	340	2	D71816	branched-chain-am
461	6	2.1	300	2	T38297	hypothetical prote	534	2.1	340	2	D64703	branched-chain-am
462	6	2.1	301	2	T29384	hypothetical prote	535	2.1	340	2	T19538	hypothetical prote
463	6	2.1	303	2	JC2410	ADP-ribosyl cyclas	536	2.1	340	2	D84109	hypothetical prote
464	6	2.1	303	2	T29383	hypothetical prote	537	2.1	341	2	S15571	cinnamyl-alcohol d
465	6	2.1	304	2	B69304	3-hydroxyacyl-CoA	538	2.1	341	2	I55623	chromoxane A2 rec
466	6	2.1	305	2	G82041	general secretion	539	2.1	341	2	F69789	hypothetical prote
467	6	2.1	305	2	G70382	phosphotidylglycer	540	2.1	341	2	AC1507	hypothetical prote

541	6	2.1	342	2	A46743	lumican precursor	614	6	2.1	369	2	AG0776	conserved hypothet
542	6	2.1	342	2	T21875	hypothetical prote	615	6	2.1	369	2	T24793	hypothetical prote
543	6	2.1	342	2	C84234	phosphate regulato	616	6	2.1	369	2	T01196	transcription fact
544	6	2.1	343	2	A49117	thromboxane A2 rec	617	6	2.1	370	2	AE0289	conserved hypothet
545	6	2.1	343	2	T69009	MHC class I Rn1 C-	618	6	2.1	372	2	S7770	probable membrane
546	6	2.1	343	2	T33945	hypothetical prote	619	6	2.1	373	2	S15161	long-chain-fatty-a
547	6	2.1	343	2	G75178	membrane protein p	620	6	2.1	374	2	S58894	hypothetical prote
548	6	2.1	344	1	A40005	hyoscyamine (6S)-d	621	6	2.1	376	2	A12176	homocitrate syntha
549	6	2.1	344	2	T12315	NADH2 dehydrogenas	622	6	2.1	376	2	AG1410	cell division prot
550	6	2.1	344	2	T12320	NADH2 dehydrogenas	623	6	2.1	376	2	T35868	probable dipeptida
551	6	2.1	344	2	T17068	NADH2 dehydrogenas	624	6	2.1	376	2	S67085	hypothetical prote
552	6	2.1	344	2	C70208	conserved hypothet	625	6	2.1	377	1	PEMOCU	gastresin (EC 3.4
553	6	2.1	345	2	T12351	NADH2 dehydrogenas	626	6	2.1	377	2	T47471	cysteine proteinas
554	6	2.1	345	2	T12362	NADH2 dehydrogenas	627	6	2.1	377	2	AE0845	probable rubredoxi
555	6	2.1	345	2	T12362	NADH2 dehydrogenas	628	6	2.1	377	2	F97267	uncharacterized co
556	6	2.1	345	2	H72488	probable anthranil	629	6	2.1	379	2	T20394	hypothetical prote
557	6	2.1	345	2	AB1837	hypothetical prote	630	6	2.1	380	2	E70181	hypothetical prote
558	6	2.1	345	2	C72760	probable heme expo	631	6	2.1	380	2	T39015	probable DNA-J-lik
559	6	2.1	346	2	A45885	MHC class I histoc	632	6	2.1	381	2	JH0152	acid phosphatase (
560	6	2.1	346	2	T19008	hypothetical prote	633	6	2.1	381	2	B48156	translation regula
561	6	2.1	346	2	AC00187	probable iron-side	634	6	2.1	382	2	C43706	nifv protein - Azo
562	6	2.1	347	2	T35518	probable secreted	635	6	2.1	382	2	AB3215	conserved hypothet
563	6	2.1	350	2	S71923	cysteine proteinas	636	6	2.1	382	2	AB0441	alkanesulfonate mo
564	6	2.1	350	2	T37511	probable phosphopr	637	6	2.1	384	2	S75683	inner membrane pro
565	6	2.1	350	2	S51494	arabinogalactan en	638	6	2.1	385	2	S29758	nifv protein - Azo
566	6	2.1	350	2	S76651	hypothetical prote	639	6	2.1	385	2	AB1656	transmembrane tran
567	6	2.1	352	2	B85709	probable DNA methy	640	6	2.1	386	2	E75588	glutaryl-CoA dehyd
568	6	2.1	352	2	D90851	probable complex	641	6	2.1	386	2	A87697	DegT/DnrJ/EryCl/St
569	6	2.1	353	2	S71338	t-complex protein	642	6	2.1	387	2	S07259	coat protein - tom
570	6	2.1	353	2	F83570	hypothetical prote	643	6	2.1	387	2	T23915	hypothetical prote
571	6	2.1	353	2	B36963	bcsA 5'-region pro	644	6	2.1	387	2	B84365	hypothetical prote
572	6	2.1	354	2	AH3092	transcription regu	645	6	2.1	388	2	A29937	Gastricin (EC 3.4
573	6	2.1	354	2	B98134	thiur protein (AF17	646	6	2.1	388	2	JC7246	pepsinogen C - com
574	6	2.1	354	2	T45837	hypothetical prote	647	6	2.1	388	2	S28798	hypothetical prote
575	6	2.1	354	2	H96928	ABC transporter, p	648	6	2.1	388	2	F70430	hypothetical prote
576	6	2.1	355	2	S17704	anthranilate phosph	649	6	2.1	389	2	A49905	protein secretion
577	6	2.1	355	2	F95979	probable transp	650	6	2.1	390	1	A39249	neutrophil cytosol
578	6	2.1	356	1	T01933	probable aldose 1-	651	6	2.1	390	2	AI3359	2-C-methyl-D-eryth
579	6	2.1	356	2	T21681	hypothetical prote	652	6	2.1	390	2	AC2761	penicillin binding
580	6	2.1	356	2	AH0088	UDP-N-acetylglucos	653	6	2.1	391	2	AB1285	transmembrane tran
581	6	2.1	357	2	T09141	cinnamyl-alcohol d	654	6	2.1	392	1	S18593	chloramphenicol re
582	6	2.1	357	2	T20029	hypothetical prote	655	6	2.1	392	2	D53240	allergen Amb a 1.4
583	6	2.1	358	2	T36415	probable iron-side	656	6	2.1	392	2	G86004	probable reverse t
584	6	2.1	358	2	D89823	hypothetical prote	657	6	2.1	393	2	B6189	protein T25N20.9 (
585	6	2.1	358	2	C82281	ferric vibriobacti	658	6	2.1	395	2	D70688	probable nitrate/n
586	6	2.1	359	2	D83103	probable phospholi	659	6	2.1	395	2	F82695	hypothetical prote
587	6	2.1	360	2	S59598	cysteine proteinas	660	6	2.1	396	2	E96911	glutamyl-tRNA redu
588	6	2.1	360	2	T34510	hypothetical prote	661	6	2.1	396	2	AG2881	HLVD family secret
589	6	2.1	360	2	UC6057	RNA-binding protei	662	6	2.1	396	2	G97657	hypothetical prote
590	6	2.1	361	2	A41535	glutamyl-peptide	663	6	2.1	397	2	F83385	probable MFS trans
591	6	2.1	362	2	T29053	branched-chain-ami	664	6	2.1	397	2	F90411	conserved hypothet
592	6	2.1	362	2	B97571	hypothetical prote	665	6	2.1	397	2	T46710	multidrug resistan
593	6	2.1	364	2	F70137	cell division prot	666	6	2.1	397	2	AE1613	multidrug-efflux t
594	6	2.1	364	2	T06507	reversibly glycosy	667	6	2.1	399	2	F83633	multidrug-efflux t
595	6	2.1	365	2	AE0259	probable phage pro	668	6	2.1	399	2	F83633	hypothetical prote
596	6	2.1	365	2	A69593	naringenin-chalcon	669	6	2.1	400	2	A87427	thiolase family pr
597	6	2.1	365	2	F64577	type I restriction	670	6	2.1	400	2	T33073	hypothetical prote
598	6	2.1	365	2	B84515	hypothetical prote	671	6	2.1	400	2	T18997	nicotinic acetylch
599	6	2.1	365	2	T06615	hypothetical prote	672	6	2.1	402	2	AI1853	sodium-dependent n
600	6	2.1	365	2	B22458	hypothetical prote	673	6	2.1	403	2	T35091	hypothetical prote
601	6	2.1	365	2	T50566	probable ABC-type	674	6	2.1	404	2	T03606	probable LfV flora
602	6	2.1	365	2	B84611	probable ubiquitin	675	6	2.1	405	2	T08521	tnlQ protein homol
603	6	2.1	365	2	A48105	probable M-factor	676	6	2.1	405	2	A25559	hypothetical prote
604	6	2.1	365	2	B97674	hypothetical prote	677	6	2.1	405	2	AG2534	hypothetical prote
605	6	2.1	367	2	S23349	hypothetical prote	678	6	2.1	406	2	T36632	probable oxidoredu
606	6	2.1	367	2	A54357	muconate cyclisom	679	6	2.1	407	2	T02670	probable thromboxa
607	6	2.1	368	2	C70786	probable ilvE prot	680	6	2.1	407	2	T00214	type II secretion
608	6	2.1	368	2	T48887	probable branched-	681	6	2.1	407	2	AE0121	probable membrane
609	6	2.1	368	2	AD2846	Ca2+/H+ antiporter	682	6	2.1	409	2	JC7293	activated T cell t
610	6	2.1	368	2	AD2899	conserved hypothet	683	6	2.1	410	2	JC4287	cytochrome P450 sc
611	6	2.1	368	2	B97623	cpaA protein (Ar00	684	6	2.1	410	2	F88978	protein F37B4.4 [i
612	6	2.1	369	2	F69478	NADH2 dehydrogenas	685	6	2.1	410	2	H71125	hypothetical prote
613	6	2.1	369	2	A53959	thromboxane A-2 re	686	6	2.1	411	2	F87644	transcription regu

687	6	2.1	411	2	F84135	multidrug-efflux t	760	2.1	453	2	B83427	pata-aminobenzoate
688	6	2.1	412	2	A82444	GDH family prote	761	2.1	453	2	E89553	D-serine/b-alanine
689	6	2.1	413	2	A2360	hypothetical prote	762	2.1	453	2	A35597	C4-dicarboxylate t
690	6	2.1	414	2	A97542	D-ala-D-ala-carbox	763	2.1	453	2	S53995	TcdX protein - Pse
691	6	2.1	414	2	E70514	probable cys22 - M	764	2.1	453	2	A59446	probable reverse t
692	6	2.1	414	2	A12544	hypothetical prote	765	2.1	454	2	A75444	hypothetical prote
693	6	2.1	414	2	H87191	low-affinity inorg	766	2.1	454	2	S77005	sensory transducti
694	6	2.1	414	2	A69907	cell wall-binding	767	2.1	454	2	C75472	probable lipase -
695	6	2.1	414	2	B96905	hypothetical prote	768	2.1	455	2	A12409	cytochrome P450 li
696	6	2.1	415	1	A83559	glutamyl-CRMA redu	769	2.1	455	2	T34412	hypothetical prote
697	6	2.1	415	2	H95412	hypothetical prote	770	2.1	456	1	I40516	spaf protein Bac
698	6	2.1	416	2	T22514	hypothetical prote	771	2.1	456	2	A84196	acyl-CoA dehydrog
699	6	2.1	417	1	A49684	gastric intrinsic	772	2.1	456	2	F83317	adenylosuccinate l
700	6	2.1	418	2	T36358	hypothetical prote	773	2.1	456	2	T51117	hypothetical prote
701	6	2.1	419	2	S54102	isopenicillin N ep	774	2.1	457	2	I73636	neuronal olfactome
702	6	2.1	419	2	B64613	hypothetical prote	775	2.1	458	2	A57397	chondroitin 6-sulf
703	6	2.1	419	2	C19000	hypothetical prote	776	2.1	458	2	T49114	hypothetical prote
704	6	2.1	421	2	F87040	conserved hypotet	777	2.1	459	2	T11084	NADH2 dehydrogenas
705	6	2.1	421	2	T25383	hypothetical prote	778	2.1	459	2	A89785	hexose phosphate t
706	6	2.1	421	2	F95371	conserved hypotet	779	2.1	460	2	A10689	probable amino aci
707	6	2.1	422	2	A71542	probable glutamate	780	2.1	460	2	A82049	conserved hypotet
708	6	2.1	423	2	C72561	hypothetical prote	781	2.1	463	2	JC2307	ribulose-bisphosph
709	6	2.1	424	2	T05775	GI/S transition co	782	2.1	463	2	D95019	hypothetical prote
710	6	2.1	425	2	I56329	gene D3 protein -	783	2.1	463	2	F83396	conserved hypotet
711	6	2.1	425	2	A37912	thrombin receptor	784	2.1	464	2	C70414	NADH2 dehydrogenas
712	6	2.1	426	2	F95846	probable ABC trans	785	2.1	464	2	E83834	flagellin BH477 l
713	6	2.1	426	2	B90410	hypothetical prote	786	2.1	464	2	F97714	hypothetical prote
714	6	2.1	427	2	H72678	hypothetical prote	787	2.1	465	2	F71213	probable H(+)-tran
715	6	2.1	427	2	S17148	alpha-thrombin rec	788	2.1	465	2	C75028	h+-transporting AT
716	6	2.1	430	2	B83572	peptidyl-prolyl ci	789	2.1	467	2	AI2231	nicotinamide nucle
717	6	2.1	430	2	B82316	hypothetical prote	790	2.1	467	2	AB3418	sensory transducti
718	6	2.1	431	2	F97318	acyl-CoA thioester	791	2.1	468	2	T07055	probable potassium
719	6	2.1	431	2	A2470	hypothetical prote	792	2.1	468	2	F84644	hypothetical prote
720	6	2.1	431	2	S09824	hypothetical prote	793	2.1	469	2	JC5741	membrane-bound pro
721	6	2.1	432	2	T17829	ankyrin repeat pro	794	2.1	470	2	F36953	dihydrolipoamide d
722	6	2.1	432	2	T08771	hypothetical prote	795	2.1	471	2	S29039	Na+-transporting A
723	6	2.1	433	2	A28055	K-kininogen, LMW I	796	2.1	471	2	AG0146	probable pyridoxal
724	6	2.1	433	2	A0909	oxaloacetate decar	797	2.1	471	2	D83388	probable MFS trans
725	6	2.1	433	2	A10508	hypothetical prote	798	2.1	472	2	AI2997	transcription regu
726	6	2.1	433	2	T39745	hypothetical prote	799	2.1	472	2	AG3600	cellulose synthase
727	6	2.1	434	2	B72228	pyrimidine-nucleos	800	2.1	473	2	F82561	hemolysin secretio
728	6	2.1	436	2	UNG591	serotonin receptor	801	2.1	473	2	B82765	conserved hypotet
729	6	2.1	436	2	A59662	UDP-N-acetylglucos	802	2.1	474	2	H90582	preprotein translo
730	6	2.1	437	2	I57942	5-hydroxytryptamin	803	2.1	474	2	T36685	probable sodium/pr
731	6	2.1	438	2	A20786	gamma-glutamyl pho	804	2.1	475	2	A81735	cysteineyl-tRNA syn
732	6	2.1	438	2	AD1886	two-component hybr	805	2.1	475	2	E84745	probable splicing
733	6	2.1	439	2	T18898	hypothetical prote	806	2.1	476	2	JC7304	gene P3 protein -
734	6	2.1	439	2	A12098	hypothetical prote	807	2.1	477	2	S01696	fatty acid hydrope
735	6	2.1	440	2	JC5520	serotonin receptor	808	2.1	477	2	AB3647	melittin resistanc
736	6	2.1	441	2	C96032	C4-dicarboxylate t	809	2.1	478	2	D96990	transmembrane prot
737	6	2.1	441	2	T24591	hypothetical prote	810	2.1	479	1	A43241	glycine hydroxymet
738	6	2.1	443	2	A00028	preprotein translo	811	2.1	479	2	B87699	conserved hypotet
739	6	2.1	443	2	D64161	hypothetical prote	812	2.1	480	2	T74228	fatty acid hydrope
740	6	2.1	443	2	T50556	stamina pistilloid	813	2.1	482	2	H98285	probable transcrip
741	6	2.1	444	2	S27384	C4-dicarboxylate t	814	2.1	483	2	T35715	export protein - S
742	6	2.1	444	2	T17855	hypothetical prote	815	2.1	483	2	S52974	regulatory protein
743	6	2.1	444	2	T19834	hypothetical prote	816	2.1	484	2	T34016	hypothetical prote
744	6	2.1	445	1	S74826	NADH2 dehydrogenas	817	2.1	484	2	E82248	fatty oxidation co
745	6	2.1	445	2	S6207	EMP47 protein prec	818	2.1	484	2	T25944	hypothetical prote
746	6	2.1	447	2	F84373	hypothetical prote	819	2.1	485	2	I73637	neuronal olfactome
747	6	2.1	448	2	AD2962	C4-dicarboxylate t	820	2.1	485	2	C75460	hypothetical prote
748	6	2.1	448	2	B98321	C4-dicarboxylate t	821	2.1	486	2	A89927	elastin binding pr
749	6	2.1	448	2	T32643	hypothetical prote	822	2.1	487	2	S54265	glycoprotein gc -
750	6	2.1	448	2	G54116	probable response	823	2.1	487	2	G83827	stage V sporulatio
751	6	2.1	448	2	D86368	hypothetical prote	824	2.1	488	2	C72334	hypothetical prote
752	6	2.1	448	2	AD1379	probable oxidoredu	825	2.1	488	2	A65344	hypothetical prote
753	6	2.1	449	2	F96852	amino acid permeas	826	2.1	488	2	F97039	glutamate synthase
754	6	2.1	449	2	S71005	glutamate transpor	827	2.1	489	2	AC1663	probable cytochrom
755	6	2.1	449	2	A33634	nitric-oxide reduc	828	2.1	490	2	T06710	probable cytochrom
756	6	2.1	450	2	F95360	probable transmemb	829	2.1	490	2	T06711	probable cytochrom
757	6	2.1	450	2	T21931	hypothetical prote	830	2.1	490	2	A87672	tldp protein limpo
758	6	2.1	451	2	H75559	conserved hypotet	831	2.1	490	2	H71480	probable GTPase/Gt
759	6	2.1	451	2	H93798	conserved hypotet	832	2.1	490	2	A81744	GTP-binding protei

833	6	2.1	491	2	AC2233	hypothetical prote	906	6	2.1	539	2	AH1035	probable phase tai
834	6	2.1	493	2	G83842	stage V sporulatio	907	6	2.1	541	1	A70022	multidrug-efflux t
835	6	2.1	494	2	S16068	testosterone 15alp	908	6	2.1	542	2	D30944	hypothetical prote
836	6	2.1	494	2	B33531	cytochrome P450 2A	909	6	2.1	542	2	H85792	hypothetical prote
837	6	2.1	494	2	A33531	testosterone 15alp	910	6	2.1	542	2	G64942	hypothetical prote
838	6	2.1	495	2	S32179	tniQ protein homol	911	6	2.1	544	2	A70155	inner membrane pro
839	6	2.1	496	2	S43114	aldenhyde dehydrog	912	6	2.1	545	2	C90047	hypothetical prote
840	6	2.1	496	2	F84664	hypothetical prote	913	6	2.1	545	2	E30460	conserved hypotnet
841	6	2.1	496	2	T30376	hypothetical prote	914	6	2.1	545	2	C95409	hypothetical prote
842	6	2.1	497	2	S75708	hypothetical prote	915	6	2.1	546	2	H72357	hypothetical prote
843	6	2.1	497	2	S22708	homeotic protein e	916	6	2.1	547	2	T23614	hypothetical prote
844	6	2.1	498	2	AH0952	conserved hypotnet	917	6	2.1	549	2	T15506	hypothetical prote
845	6	2.1	499	2	S46560	wetA protein - Pen	918	6	2.1	551	2	A49904	L-lactate permease
846	6	2.1	501	2	T44298	sodium/proline sym	919	6	2.1	551	2	A98189	L-lactate permease
847	6	2.1	502	1	D64110	lysine-tRNA ligase	920	6	2.1	551	2	B86036	protein-tyrosine-p
848	6	2.1	502	1	ACHU47	nicotinic acetylch	921	6	2.1	552	2	S56283	hypothetical prote
849	6	2.1	502	2	JN0113	nicotinic acetylch	922	6	2.1	552	2	A99493	hypothetical prote
850	6	2.1	502	2	G02259	alpha 7 neuronal n	923	6	2.1	553	2	E95160	hypothetical prote
851	6	2.1	502	2	T25669	hypothetical prote	924	6	2.1	553	2	D98026	hypothetical prote
852	6	2.1	503	2	E82730	peptide synthase X	925	6	2.1	554	2	D72760	hypothetical prote
853	6	2.1	504	2	T37984	probable homoserin	926	6	2.1	554	2	H71128	hypothetical prote
854	6	2.1	504	2	E64118	sodium/proline sym	927	6	2.1	555	2	S63177	hypothetical prote
855	6	2.1	505	2	T10896	cytochrome P450 (E	928	6	2.1	557	2	B28182	mannosyl transfera
856	6	2.1	505	2	D96672	probable Cytochrom	929	6	2.1	558	2	S71337	hemolysin B - Serr
857	6	2.1	506	2	H83831	sopre Germination	930	6	2.1	559	2	T23571	t-complex protein
858	6	2.1	506	2	B87102	conserved membrane	931	6	2.1	560	2	T14616	hypothetical prote
859	6	2.1	506	2	T40396	glucosyltransferas	932	6	2.1	561	2	A52649	alpha-glucosidase
860	6	2.1	506	2	H91214	probable 2-compone	933	6	2.1	561	2	AH0452	hypothetical prote
861	6	2.1	506	2	T47184	hypothetical prote	934	6	2.1	562	2	C84721	hemolysin activato
862	6	2.1	506	2	A86051	probable 2-compone	935	6	2.1	563	2	S32156	mandelonitrile lya
863	6	2.1	506	2	C65178	hypothetical 57.4	936	6	2.1	564	2	H82539	ABC transporter At
864	6	2.1	507	2	S33921	alpha-amylase (EC	937	6	2.1	564	2	E82539	transmembrane rece
865	6	2.1	510	2	A96673	probable cytochrom	938	6	2.1	566	2	F70028	probable membrane
866	6	2.1	510	2	AG1539	oligo-1,6-glucosid	939	6	2.1	566	2	S28068	mxid protein - Shi
867	6	2.1	511	2	B88381	probable cytochrom	940	6	2.1	570	2	F87446	potassium-transport
868	6	2.1	511	2	H96672	probable cytochrom	941	6	2.1	571	2	G90891	probable sulfatase
869	6	2.1	511	2	T10964	inositol-3-phospha	942	6	2.1	571	2	B85726	probable sulfatase
870	6	2.1	511	2	T04221	hypothetical prote	943	6	2.1	571	2	E64903	arylsulfatase homo
871	6	2.1	512	2	H84501	probable cytochrom	944	6	2.1	573	2	T07948	mandelonitrile lya
872	6	2.1	516	2	T06716	hypothetical prote	945	6	2.1	573	2	AG2133	ATP-binding protei
873	6	2.1	516	2	JE0286	L-amino-acid oxida	946	6	2.1	574	2	H86467	probable transcrip
874	6	2.1	517	2	S69347	steroid libeta-mon	947	6	2.1	575	2	G75282	probable glucathi
875	6	2.1	518	2	H64775	probable membrane	948	6	2.1	575	2	B71420	hypothetical prote
876	6	2.1	518	2	B85543	hypothetical prote	949	6	2.1	576	2	T01229	probable membrane
877	6	2.1	518	2	F90692	hypothetical prote	950	6	2.1	577	2	S46613	hypothetical prote
878	6	2.1	520	2	AT3596	sugar transport At	951	6	2.1	578	2	T01229	hypothetical prote
879	6	2.1	521	1	VHBPT4	major capsid prote	952	6	2.1	579	2	A56740	sparm-egg recognit
880	6	2.1	521	2	T35832	probable integral	953	6	2.1	580	2	B38418	jockey protein 1 -
881	6	2.1	521	2	E95052	hypothetical prote	954	6	2.1	581	2	S44896	ZK1236.1 protein -
882	6	2.1	523	2	S53401	probable membrane	955	6	2.1	581	2	A97119	probable membrane
883	6	2.1	524	1	DBYCG6	glucose-6-phosphat	956	6	2.1	581	2	S46742	hypothetical prote
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885	6	2.1	525	2	S03600	cell surface antig	958	6	2.1	583	2	JC6504	alpha,alpha-trehal
886	6	2.1	526	2	S03600	cell surface antig	959	6	2.1	583	2	B82744	conserved hypotnet
887	6	2.1	527	2	S64702	cell surface antig	960	6	2.1	586	2	T12886	conserved hypotnet
888	6	2.1	527	2	T39263	chaperonin subunit	961	6	2.1	586	2	A82350	conserved phosphol
889	6	2.1	527	2	T37055	probable oxidoredu	962	6	2.1	590	2	F95853	probable phosphol
890	6	2.1	527	2	T25131	hypothetical prote	963	6	2.1	590	2	D85063	hypothetical prote
891	6	2.1	528	2	C85056	probable DNA-bind	964	6	2.1	591	2	T13650	zinc finger protei
892	6	2.1	528	1	SAHUF4	cell surface antig	965	6	2.1	591	2	T13650	serine/threonine p
893	6	2.1	529	2	H70744	hypothetical prote	966	6	2.1	592	2	T42078	uroporphyrinogen m
894	6	2.1	532	2	T07927	protein disulfide-	967	6	2.1	593	2	S38145	A kinase anchor pr
895	6	2.1	532	2	T28784	hypothetical prote	968	6	2.1	593	2	I35173	probable alpha-glu
896	6	2.1	533	2	E84858	phosphoprotein pho	969	6	2.1	594	2	D97431	pyruvate decarboxy
897	6	2.1	533	2	UC2285	preprotein translo	970	6	2.1	594	2	T38114	hypothetical prote
898	6	2.1	533	2	H70735	hypothetical prote	971	6	2.1	594	2	T23841	flagellin - Escher
899	6	2.1	533	2	G72593	hypothetical prote	972	6	2.1	595	2	A48658	flagellin - Escher
900	6	2.1	535	2	G57235	CTP synthase (UTP-	973	6	2.1	595	2	B48658	hypothetical prote
901	6	2.1	536	2	H82880	probable ABC subst	974	6	2.1	595	2	S75439	hypothetical prote
902	6	2.1	537	1	YMSB6	tyrosinase-related	975	6	2.1	595	2	T04438	hypothetical prote
903	6	2.1	537	2	C97765	CTP synthase (EC 6	976	6	2.1	597	2	E70928	hypothetical prote
904	6	2.1	538	2	AC1850	NADH dehydrogenase	977	6	2.1	600	2	T50799	serine/threonine p
905	6	2.1	538	2	S57766	RNA-export mediato	978	6	2.1	600	2	T02692	hypothetical prote

979 6 2.1 601 2 AH1003 glutathione-regula
 980 6 2.1 602 2 T45386 endopeptidase IV [
 981 6 2.1 604 2 C87818 protein glh-1 (imp
 982 6 2.1 604 2 T15132 ATP-dependent RNA
 983 6 2.1 605 2 D83007 regulatory protein
 984 6 2.1 606 2 AH2485 hypothetical prote
 985 6 2.1 608 2 S76192 hypothetical prote
 986 6 2.1 609 2 T04946 hypothetical prote
 987 6 2.1 610 2 T23836 hypothetical prote
 988 6 2.1 613 1 S74461 ABC transporter sl
 989 6 2.1 614 2 H83978 GTP-binding protei
 990 6 2.1 618 2 S33044 hypothetical prote
 991 6 2.1 620 1 W2BEC1 gene 28 protein -
 992 6 2.1 620 2 S19660 dnaK-type molecula
 993 6 2.1 620 2 S73236 dnaK-type molecula
 994 6 2.1 621 2 A84933 glutamine-fructose
 995 6 2.1 621 2 A83016 Na+/H+ antiporter
 996 6 2.1 622 2 G81981 probable lipopolys
 997 6 2.1 623 2 I46382 Zfp precursor - mo
 998 6 2.1 623 2 B81037 lipopolysaccharide
 999 6 2.1 624 2 A55576 collagen alpha 2(X
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ALIGNMENTS

RESULT 1
 B38290
 GRO-gamma precursor - human
 N;Alternate names: growth-regulated protein gamma; macrophage inflammatory protein 2 beta
 C;Species: Homo sapiens (man)
 C;Date: 31-May-1991 #sequence_revision 27-Oct-1995 #text_change 20-Aug-1999
 A;Accession: JH0282; B38290; C46519
 R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
 J. Exp. Med. 172, 911-919, 1990
 A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
 A;Reference number: JH0200; MUID:90354792; PMID:2201751
 A;Accession: JH0282
 A;Molecule type: mRNA
 A;Residues: 1-107 <TEK>
 A;Cross-references: GB:X53800; NID:G34662; PIDN:CAA37809.1; PID:G34663
 R;Haskill, S.; Pearce, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
 A;Title: Identification of three related human GRO genes encoding cytokine functions.
 A;Reference number: A38290; MUID:91017578; PMID:2217207
 A;Accession: B38290
 A;Molecule type: mRNA
 A;Residues: 1-26,'G',29-107 <HAS>
 A;Cross-references: GB:M36821; NID:G183632; PIDN:AAA63184.1; PID:G183633
 R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
 J. Immunol. 150, 1000-1010, 1993
 A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tu
 A;Reference number: A46519; MUID:93139489; PMID:8423327
 A;Accession: C46519
 A;Molecule type: protein
 A;Residues: 35-52 <PRO>
 A;Experimental source: MG-63 osteosarcoma cells
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QY 167 LLLLVAAAS 174
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 Db 22 LLLLVAAAS 29

RESULT 2
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 macrophage inflammatory protein 2 alpha precursor - human
 N;Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
 C;Accession: JH0281; A35931; A38290; A60407
 R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
 J. Exp. Med. 172, 911-919, 1990
 A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
 A;Reference number: JH0200; MUID:90354792; PMID:2201751
 A;Accession: JH0281
 A;Molecule type: mRNA
 A;Residues: 1-107 <TEK>
 A;Cross-references: GB:X53799; NID:G34658; PIDN:CAA37808.1; PID:G34659
 R;Iida, N.; Grotenhorst, G.R.
 Mol. Cell. Biol. 10, 5596-5599, 1990
 A;Title: Cloning and sequencing of a new gro transcript from activated human monocytes:
 A;Reference number: A35931; MUID:90377259; PMID:2078213
 A;Accession: A35931
 A;Molecule type: mRNA
 A;Residues: 1-107 <IID>
 A;Cross-references: GB:M57731; GB:M36964; NID:G183626; PIDN:AAA63182.1; PID:G183627
 R;Haskill, S.; Pearce, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; N
 Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
 A;Title: Identification of three related human GRO genes encoding cytokine functions.
 A;Reference number: A38290; MUID:91017578; PMID:2217207
 A;Accession: A38290
 A;Molecule type: mRNA
 A;Residues: 1-107 <HAS>
 A;Cross-references: GB:M36820; NID:G183628; PIDN:AAA63183.1; PID:G183629
 R;Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskill,
 J. Immunol. 144, 4434-4441, 1990
 A;Title: Monocyte adherence results in selective induction of novel genes sharing homolo
 A;Reference number: A60407; MUID:90257367; PMID:2341726
 A;Accession: A60407
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 56-107 <SPO>
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 C;Keywords: inflammation
 F;1-34/Domain: signal sequence #status predicted <SIG>
 F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>
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 Db 22 LLLLVAAAS 29

RESULT 3
 AI2439
 hypothetical protein all5073 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AI2439
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AI2439
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-475 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA076772.1; PID:G17134211; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: all5073

Query Match 2.8%; Score 8; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTYLLLF 11
Db 130 LTYLLLF 137

RESULT 4
C90171
RNase L inhibitor [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: C90171
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90171
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-600 <KUR>
A:Cross-references: GB:AE006641; NID:gl3813430; PIDN:AAK40626.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS00287
C:Superfamily: ribonuclease L inhibitor; ATP-binding cassette homology; ferredoxin 2[4Fe

Query Match 2.8%; Score 8; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LLVAASLL 176
Db 221 LLVAASLL 228

RESULT 5
C30552
macrophage inflammatory protein 1-beta precursor - mouse
N:Alternate names: H400; SIS gamma; T-cell activation protein gamma
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 16-Jul-1999
C:Accession: C30552; J00088; P50304; S22042
R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a ne
s of various activation processes.
A:Reference number: A30552; MUID:89093958; PMID:2521353
A:Accession: C30552
A:Molecule type: mRNA
A:Residues: 1-92 <BRO>
A:Cross-references: GB:M23503; NID:g533244; PIDN:AAA40148.1; PID:g533245
R:Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas
J. Exp. Med. 168, 2251-2259, 1998
A:Title: Resolution of the two components of macrophage inflammatory protein 1, and clon
A:Reference number: J00088; MUID:89067830; PMID:3058856
A:Accession: J00088
A:Molecule type: mRNA
A:Residues: 1-92 <SHE>
A:Cross-references: GB:M35590; NID:g199696; PIDN:AAA39708.1; PID:g199697
A:Accession: P50304
A:Molecule type: protein
A:Residues: 24-33, 'XX', '36', 'X', '38' <SH2>
R:Daubersies, P.; Lepretre, P.; Bailleul, B.; Grove, M.; Pragnell, I.; Plumb, M.
submitted to the EMBL Data Library, October 1991
A:Description: Sequence of the murine macrophage inflammatory protein 1b gene.
A:Reference number: S22042
A:Accession: S22042
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-92 <DAU>
A:Cross-references: EMBL:X62502; NID:g53126; PIDN:CAA44364.1; PID:g53127
C:Comment: This protein is a monokine.
C:Genetics:
A:Introns: 26/1; 64/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>
F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
Db 10 LLLLVAA 16

RESULT 6
D90259
hypothetical protein SSO1068 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: D90259
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90259
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <KUR>
A:Cross-references: GB:AE006641; NID:gl3814257; PIDN:AAK41331.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1068

Query Match 2.4%; Score 7; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLLTLYL 8
Db 68 PLLTLYL 74

RESULT 7
A28414
melanoma growth-stimulatory activity precursor - human
N:Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha; gr
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C:Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
R:Baker, N.E.; Kucera, G.; Richmond, A.
Nucleic Acids Res. 18, 6453, 1990
A:Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) ge
A:Reference number: S13669; MUID:91057157; PMID:2129556
A:Accession: S13669
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <BAK>
A:Cross-references: EMBL:X54489; NID:g34625; PIDN:CRA38361.1; PID:g34626
R:Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A:Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A:Reference number: A94184; MUID:88041072; PMID:890161
A:Accession: A28414
A:Molecule type: mRNA
A:Residues: 1-107 <ANI>

A;Cross-references: GB:J03561; NID:g183622; PIDN:AAA35933.1; PID:g306806
 R;Richmond, A.; Balenien, E.; Thomas, H.G.; Flaggs, G.; Barton, D.E.; Spiess, J.; Bordo
 EMBO J. 7, 2025-2033, 1988
 A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimulat
 A;Reference number: S00983; MUID:88328991; PMID:2970963
 A;Accession: S00983
 A;Molecule type: mRNA
 A;Residues: 1-107 <RIC>
 A;Cross-references: EMBL:X12510; NID:g34621; PIDN:CAA31027.1; PID:g34622
 R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
 J. Immunol. 144, 2223-2232, 1990
 A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-
 A;Reference number: A60401; MUID:90187866; PMID:2179408
 A;Accession: B60401
 A;Molecule type: protein
 A;Residues: 35-42, 'X', 44, 'X', 46-48 <SCH>
 A;Experimental source: dermal fibroblasts
 R;Golds, E.B.; Mason, P.; Nyirkos, P.
 Biochem. J. 259, 585-588, 1989
 A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neut
 A;Reference number: S03975; MUID:89246368; PMID:2655583
 A;Accession: S03976
 A;Molecule type: protein
 A;Residues: 35-41, 'X', 43-49, 'X', 51-52, 'XX', 55-57 <GOL>
 R;Schroeder, J.M.; Persoon, N.L.M.; Christophers, E.
 J. Exp. Med. 171, 1091-1100, 1990
 A;Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil-ad
 nity with melanoma growth stimulatory activity.
 A;Reference number: A47626; MUID:90217938; PMID:2182761
 A;Accession: A47626
 A;Molecule type: protein
 A;Residues: 35-63, 'X', 65 <SC2>
 A;Experimental source: LPS-stimulated monocytes
 R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
 J. Immunol. 150, 1000-1010, 1993
 A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tu
 A;Reference number: A46519; MUID:93139489; PMID:8423327
 A;Accession: B46519
 A;Molecule type: protein
 A;Residues: 35-62 <PRO>
 A;Experimental source: MG-63 osteosarcoma cells
 C;Genetics:
 A;Gene: GDB:GROI
 A;Cross-references: GDB:120181; OMIM:155730
 A;Map position: 4q21-4q21
 C;Superfamily: beta-thromboglobulin
 F;1-34/Domain: signal sequence #status predicted <SIG>
 F;35-107/Product: melanoma growth-stimulatory activity #status experimental <MAT>

Query Match 2.4%; Score 7; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
 |||||
 Db 22 LLLLVAA 28

RESULT 8
 149011
 Gene Ubely protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 A;Reference number: I49011
 A;Accession: I49011
 R;Chang, B.H.; Li, W.H.
 J. Mol. Evol. 40, 70-77, 1995
 A;Title: Estimating the intensity of male-driven evolution in rodents by using X-linked
 A;Reference number: I49010; MUID:95230700; PMID:7714913
 A;Accession: I49011
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-109 <RES>
 A;Cross-references: EMBL:U09052; NID:g710299; PIDN:AAC52170.1; PID:g710300

Query Match 2.4%; Score 7; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
 |||||
 Db 22 LLLLVAA 28

RESULT 8
 149011
 Gene Ubely protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 A;Reference number: I49011
 A;Accession: I49011
 R;Chang, B.H.; Li, W.H.
 J. Mol. Evol. 40, 70-77, 1995
 A;Title: Estimating the intensity of male-driven evolution in rodents by using X-linked
 A;Reference number: I49010; MUID:95230700; PMID:7714913
 A;Accession: I49011
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-109 <RES>

C;Genetics:
 A;Gene: Ubely
 A;Introns: 14/2; 79/3; 104/3
 C;Superfamily: ubiquitin-activating enzyme E1

Query Match 2.4%; Score 7; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TIQLAGT 215
 |||||
 Db 22 TIQLAGT 28

RESULT 9
 163169
 Gene Ubely protein - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
 C;Accession: I63169
 R;Chang, B.H.; Li, W.H.
 J. Mol. Evol. 40, 70-77, 1995
 A;Title: Estimating the intensity of male-driven evolution in rodents by using X-linked
 A;Reference number: I49010; MUID:95230700; PMID:7714913
 A;Accession: I63169
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-109 <RES>
 A;Cross-references: EMBL:U09056; NID:g710305; PIDN:AAC52172.1; PID:g710306
 C;Genetics:
 A;Gene: Ubely
 A;Introns: 14/2; 79/3; 104/3
 C;Superfamily: ubiquitin-activating enzyme E1

Query Match 2.4%; Score 7; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TIQLAGT 215
 |||||
 Db 22 TIQLAGT 28

RESULT 10
 B70401
 Hypothetical protein aq1176 - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
 C;Accession: B70401
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
 V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: B70401
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-111 <AQF>
 A;Cross-references: GB:AE000727; NID:g2983623; PIDN:AAC07206.1; PID:g2983638; GB:AE00065
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: aq1176
 C;Superfamily: Aquifex aeolicus hypothetical protein aq_1176

Query Match 2.4%; Score 7; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 DQVEVEY 236
 |||||
 Db 38 DQVEVEY 44

RESULT 11
A87594
bleomycin resistance protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A87594
R:Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87594
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <STO>
A:Cross-references: GB:AE005673; NID:gl3424385; PIDN:AAK24749.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2785

Query Match 2.4%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 LERGSLT 37
Db 38 LERGSLT 44

RESULT 12
C81087
hypothetical protein NMB1406 [imported] - *Neisseria meningitidis* (strain MC58 serogroup
C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81087
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: C81087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <TET>
A:Cross-references: GB:AE002489; GB:AE002098; NID:g7226640; PIDN:AAF41769.1; PID:g722664
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1406

Query Match 2.4%; Score 7; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 LPLIFTI 165
Db 80 LPLIFTI 86

RESULT 13
D82105
conserved hypothetical protein VC2206 [imported] - *Vibrio cholerae* (strain N16961 serog
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82105
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82105

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <HEI>
A:Cross-references: GB:AE004292; GB:AE003852; NID:g9656760; PIDN:AAF95351.1; GSPDB:GN0014
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2206
A:Map position: 1

Query Match 2.4%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVAA 173
Db 6 LLLVAA 12

RESULT 14
B44827
FMRamide-like peptide - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B44827
R:Rosoff, M.L.; Burglin, T.R.; Li, C.
J. Neurosci. 12, 2356-2361, 1992
A:Title: Alternatively spliced transcripts of the flp-1 gene encode distinct FMRamide-1
A:Reference number: A44827; MUID:92300457; PMID:1607945
A:Accession: B44827
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-164 <ROS>
A:Notes: sequence extracted from NCBI backbone (NCBIP:106594)
C:Keywords: neuropeptide

Query Match 2.4%; Score 7; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 LLLVAA 173
Db 9 LLLVAA 15

RESULT 15
C86241
protein T16B5.9 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C86241
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <STO>
A:Cross-references: GB:AE005172; NID:g4874271; PIDN:AAD31336.1; GSPDB:GN00141
C:Genetics:
A:Gene: T16B5.9
A:Map position: 1

Query Match 2.4%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 TSPRAT 221
| | | | |
Db 55 TSPRAT 61

Search completed: September 16, 2004, 12:57:33
Job time : 63 secs

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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:40:41 ; Search time 24 Seconds
(without alignments)
629.181 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290

Sequence: 1 MPLILYLLFLWLSGYSIAT.....SXLPGRGPPEPTETYSIRP 290

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.8	107	1 M12A HUMAN	P19875 homo sapien
2	8	2.8	107	1 M12B HUMAN	P19876 homo sapien
3	7	2.4	92	1 SY04 MOUSE	P14097 mus musculus
4	7	2.4	92	1 SY04 RAT	P50230 rattus norv
5	7	2.4	98	1 GROG BOVIN	O46675 bos taurus
6	7	2.4	103	1 GRO SHEEP	O46678 ovis aries
7	7	2.4	104	1 GRO2 BOVIN	P47854 oryctolagus
8	7	2.4	104	1 GROB BOVIN	O46677 bos taurus
9	7	2.4	107	1 GRO HUMAN	P09341 homo sapien
10	7	2.4	111	1 YB76 AQUAE	O67237 aquifex aeo
11	7	2.4	160	1 LY96 CRIGR	P58755 cricetus
12	7	2.4	171	1 YW87 PSEAE	P58756 pseudomonas
13	7	2.4	175	1 RRP CAEEL	P41855 caenorhabdi
14	7	2.4	185	1 RRP NEIMA	Q91952 neisseria m
15	7	2.4	200	1 HA19 MOUSE	P14431 mus musculus
16	7	2.4	255	1 Y01X BACSU	P54535 bacillus su
17	7	2.4	258	1 ETXG STAM	O85382 staphylococ
18	7	2.4	268	1 CS28 PEA	P27490 pisum sativ
19	7	2.4	326	1 HA18 MOUSE	P14430 mus musculus
20	7	2.4	327	1 TAL CHLCV	Q822J3 chlamydophi
21	7	2.4	334	1 HA17 MOUSE	P14429 mus musculus
22	7	2.4	335	1 VMSA HPBHE	P13847 heron hepat
23	7	2.4	357	1 DCUP MYCTU	O53231 mycobacteri
24	7	2.4	361	1 QPCT HUMAN	Q16769 homo sapien
25	7	2.4	362	1 QREA DELRA	Q8rul9 deinoococcus
26	7	2.4	397	1 ARGJ THENA	Q9x2a3 t arginine
27	7	2.4	400	1 BJAR MOUSE	P25962 mus musculus
28	7	2.4	401	1 BJAR RAT	P26255 rattus norv
29	7	2.4	425	1 PURA FUSNN	P58793 fusobacteri
30	7	2.4	425	1 PURA FUSNU	O68581 fusobacteri
31	7	2.4	442	1 URAY MOUSE	P11254 mus musculus
32	7	2.4	461	1 TIPI SCHPO	P79065 schizosacch
33	7	2.4	462	1 VATB_PIRFU	Q8u4a5 pyrococcus

34	7	2.4	484	1	VL55 CAEEB
35	7	2.4	513	1	CATB_PSEAE
36	7	2.4	521	1	VGLC_HSVBC
37	7	2.4	560	1	ANNS_CRIGR
38	7	2.4	560	1	ASNS_MOUSE
39	7	2.4	560	1	ASNS_RAT
40	7	2.4	592	1	SYR_COXBU
41	7	2.4	617	1	ESR1 ICTPU
42	7	2.4	622	1	GLMS_CORGL
43	7	2.4	634	1	SL56_RAT
44	7	2.4	635	1	SL56_HUMAN
45	7	2.4	636	1	SL56_RABIT
46	7	2.4	694	1	PKC9_MOUSE
47	7	2.4	697	1	SM2A_SCHGR
48	7	2.4	709	1	CN1C_HUMAN
49	7	2.4	716	1	HEPA_HSVEB
50	7	2.4	725	1	AGA1_YEAST
51	7	2.4	744	1	REP1_HUMAN
52	7	2.4	813	1	AD33_HUMAN
53	7	2.4	911	1	B3AT_HUMAN
54	7	2.4	968	1	KBF1_HUMAN
55	7	2.4	971	1	KBF1_MOUSE
56	7	2.4	1011	1	M3K6_HUMAN
57	7	2.4	1047	1	ANP8_HUMAN
58	7	2.4	1065	1	SED4_YEAST
59	7	2.4	1087	1	AKA9_RABIT
60	7	2.4	1099	1	CYA7_MOUSE
61	7	2.4	1159	1	SOR2_MOUSE
62	7	2.4	1171	1	GLG1_RAT
63	7	2.4	1219	1	SOR3_MOUSE
64	7	2.4	1365	1	YAK1_SCHPO
65	7	2.4	1400	1	RON_HUMAN
66	7	2.4	2491	1	MPRI_HUMAN
67	6	2.1	36	1	PSBY_ODOSI
68	6	2.1	47	1	YRR7_MYCCA
69	6	2.1	54	1	SASG_BACPF
70	6	2.1	59	1	Y586_PYRAE
71	6	2.1	64	1	SCX5_ANDMA
72	6	2.1	64	1	SCX5_LEIQU
73	6	2.1	76	1	RCRO_BPHKO
74	6	2.1	86	1	GON2_CLAGA
75	6	2.1	92	1	RS19_SYNY3
76	6	2.1	99	1	RS10_HALMA
77	6	2.1	99	1	SY08_BOVIN
78	6	2.1	103	1	SLUR_HUMAN
79	6	2.1	103	1	VGG_EPBST1
80	6	2.1	104	1	GROA_BOVIN
81	6	2.1	106	1	YFD2_YEAST
82	6	2.1	112	1	N1FW_RHOC
83	6	2.1	112	1	ACPM_MYCTU
84	6	2.1	115	1	E313_ADECG
85	6	2.1	117	1	SY24_MOUSE
86	6	2.1	119	1	RNP_MESAU
87	6	2.1	124	1	Y670_PASMAU
88	6	2.1	124	1	CRCB_CAUCR
89	6	2.1	127	1	HIS3_STRCO
90	6	2.1	128	1	YF75_MYCPN
91	6	2.1	130	1	RNP_CRILLO
92	6	2.1	131	1	MPZ2_MOUSE
93	6	2.1	137	1	PSIE_LISIN
94	6	2.1	137	1	PSIE_LISMO
95	6	2.1	139	1	IL5_MACEU
96	6	2.1	147	1	HEMT_METJA
97	6	2.1	151	1	SOD1_LYCES
98	6	2.1	151	1	SOD2_LYCES
99	6	2.1	153	1	UBCC_YEAST
100	6	2.1	153	1	NU6M_CANPA
101	6	2.1	156	1	RS7_STRCO
102	6	2.1	156	1	RS7_STRRP
103	6	2.1	156	1	Y003_METJA
104	6	2.1	160	1	YVYG_BACSU
105	6	2.1	163	1	ILVH_ECOLI
106	6	2.1	163	1	ILVH_SALTY

107	6	2.1	170	1	ARGR MYCTU	P94992 mycobacteri	180	6	2.1	274	1	YX1 CVHSA	P59632 human coron
108	6	2.1	171	1	COX5 NEUCR	P06810 neurospora	181	6	2.1	275	1	YMA9 CAEBL	P34454 caenorhabdi
109	6	2.1	171	1	Y762 ARCFU	O29496 archaeoglob	182	6	2.1	280	1	PANB MYCVN	Q917b2 mycobacteri
110	6	2.1	171	1	YX71 YEAST	P35652 saccharomyc	183	6	2.1	281	1	PANB MYCTU	Q10505 mycobacteri
111	6	2.1	173	1	PYR STRP3	Q8K75 streptococc	184	6	2.1	283	1	VNS4 MSTV	P33521 maize strip
112	6	2.1	173	1	PYR STRP8	P59013 streptococc	185	6	2.1	284	1	DRN1 MOUSE	P43183 mus musculu
113	6	2.1	173	1	PYR STRP9	Q9a0d0 streptococc	186	6	2.1	285	1	DDH2 HUMAN	Q95865 homo sapien
114	6	2.1	187	1	VGG BPA13	P1281 bacterioph	187	6	2.1	286	1	PANB MYCLE	Q9fhd5 arabidopsis
115	6	2.1	187	1	VGG BPHK	Q38042 bacterioph	188	6	2.1	286	1	UDU1 ARATH	P34961 rice stripe
116	6	2.1	188	1	C561 ECOLI	P75925 escherichia	189	6	2.1	286	1	VNS4 RSMV	Q00847 rice stripe
117	6	2.1	192	1	LUM RABIT	O46373 oryctolagus	190	6	2.1	286	1	VNS4 BSVT	P34961 rice stripe
118	6	2.1	192	1	Y541 PSESM	Q8a56 pseudomonas	191	6	2.1	289	1	BSN1 BACSU	Q03091 bacillus su
119	6	2.1	193	1	HS CAMO	P06513 calina mos	192	6	2.1	289	1	QCRC MYCLE	C69583 mycobacteri
120	6	2.1	193	1	MOBA RHOSH	P95645 rhodobacter	193	6	2.1	292	1	U714 HUMAN	P50876 homo sapien
121	6	2.1	197	1	T485 HUMAN	O14894 homo sapien	194	6	2.1	292	1	U714 MOUSE	Q925f3 mus musculu
122	6	2.1	197	1	VR26 NPVP	O10276 orgyia pseu	195	6	2.1	294	1	CAMG MOUSE	P49070 mus musculu
123	6	2.1	198	1	YXKL PORPU	P51354 porphyra pu	196	6	2.1	296	1	CAMG HUMAN	P49069 homo sapien
124	6	2.1	200	1	YXKL LOTJA	Q9bbr3 lotus japon	197	6	2.1	299	1	CRX BOVIN	Q9xsk0 bos taurus
125	6	2.1	202	1	SODP FEA	P11964 pisum sativ	198	6	2.1	299	1	CRX HUMAN	O43186 homo sapien
126	6	2.1	202	1	WR59 ARATH	Q9e509 arabidopsis	199	6	2.1	299	1	CRX MOUSE	O54751 mus musculu
127	6	2.1	206	1	YQII BACSU	P54525 bacillus su	200	6	2.1	301	1	CTFS HUMAN	Q9uja2 homo sapien
128	6	2.1	208	1	YM16 YEAST	P40608 saccharomyc	201	6	2.1	303	1	CD38 RAT	Q64244 rattus norv
129	6	2.1	211	1	MOTX VIBPA	P40608 vibrio para	202	6	2.1	303	1	CTFS MOUSE	Q802m8 mus musculu
130	6	2.1	211	1	SODP ORYSA	P93407 oryza sativ	203	6	2.1	305	1	GSPC VIBCH	P45777 vibrio chol
131	6	2.1	212	1	ATP6 TROHI	O03570 tropidurus	204	6	2.1	306	1	PRVA ANASP	Q8yvt3 anabaena sp
132	6	2.1	212	1	ATP6 TROMO	O03359 tropidurus	205	6	2.1	306	1	YLIC SCOLI	P75798 escherichia
133	6	2.1	212	1	Y330 STRA3	P59254 streptococc	206	6	2.1	308	1	Y04F MYCTU	Q10786 mycobacteri
134	6	2.1	214	1	DSBA PSESM	O52376 pseudomonas	207	6	2.1	309	1	YQGH BACSU	P46339 bacillus su
135	6	2.1	215	1	O2A6 HUMAN	Q96r47 homo sapien	208	6	2.1	311	1	FMT STRP6	Q8dmr7 streptococc
136	6	2.1	216	1	E325 ADECC	Q65959 canine aden	209	6	2.1	311	1	FMT STRP6	Q8dmr7 streptococc
137	6	2.1	216	1	SODP ARATH	O78310 arabidopsis	210	6	2.1	311	1	YCAV CLOKL	P38943 clostridium
138	6	2.1	216	1	SODP ZANAE	O65175 zantedeschi	211	6	2.1	312	1	DRBX ANAPL	O57314 anas platyr
139	6	2.1	217	1	O2A5 HUMAN	Q96r48 homo sapien	212	6	2.1	313	1	PRRB RHIME	Q92q15 rhizobium m
140	6	2.1	217	1	SODP LYCES	P14831 lycopersico	213	6	2.1	314	1	MER2 YEAST	P21651 saccharomyc
141	6	2.1	220	1	SODP SOLCS	O04997 solidago ca	214	6	2.1	314	1	YP69 MYCTU	Q50652 mycobacteri
142	6	2.1	220	1	VM02 VACC	P21092 vaccinia vi	215	6	2.1	315	1	O3A2 HUMAN	P47893 homo sapien
143	6	2.1	221	1	NUSB SYN33	P74395 synechocyst	216	6	2.1	318	1	MYOD RAT	Q02346 rattus norv
144	6	2.1	221	1	TVSY METH	Q26868 methanobact	217	6	2.1	318	1	Y391 BUCBP	O89ac3 buchnera ap
145	6	2.1	222	1	SODP SPIOL	P07505 spinacia ol	218	6	2.1	319	1	CU06 HUMAN	P57060 homo sapien
146	6	2.1	222	1	Y5Y1 METIM	P80305 methanobact	219	6	2.1	320	1	YC55 PORPU	P51203 porphyra pu
147	6	2.1	226	1	GSPB AERHY	P45755 aeromonas h	220	6	2.1	322	1	FSA BRARE	Q99yva brachydanio
148	6	2.1	229	1	CEMA ATREE	Q8s8w5 atropa bell	221	6	2.1	322	1	HEM3 CAUCR	Q9abz8 caulobacter
149	6	2.1	229	1	CMA LOTJA	P58155 lotus japon	222	6	2.1	327	1	OPT CANFA	P33286 canis famli
150	6	2.1	229	1	CMA SOYBN	P49160 glycine max	223	6	2.1	330	1	PRC3 PORGI	P33437 porphyromon
151	6	2.1	229	1	CMA TOBAC	P12213 nicotiana t	224	6	2.1	331	1	LDHC HUMAN	P07864 homo sapien
152	6	2.1	230	1	YGTQ ECOLI	P42598 escherichia	225	6	2.1	334	1	PRC1 PORGI	P59916 porphyromon
153	6	2.1	231	1	PCAT PSEPU	Q01103 pseudomonas	226	6	2.1	335	1	DUSA SHEON	Q8aa10 shewanella
154	6	2.1	231	1	Y236 CAMUE	Q9piq8 campylobact	227	6	2.1	335	1	ZDH1 STAAM	Q99581 staphylococ
155	6	2.1	235	1	HG12 CAEBL	Q09390 caenorhabdi	228	6	2.1	335	1	ZDH1 STAAM	Q8nvd1 staphylococ
156	6	2.1	236	1	STX8 HUMAN	P11642 maize chlor	229	6	2.1	336	1	NOSO BACSU	Q34453 bacillus su
157	6	2.1	236	1	STX8 HUMAN	Q9smh2 castanea sa	230	6	2.1	336	1	ZDH1 STAEP	Q8crj7 staphylococ
158	6	2.1	236	1	STX8 RAT	Q9unk0 homo sapien	231	6	2.1	337	1	CMST HUMAN	P78382 homo sapien
159	6	2.1	237	1	ATP6 PETVA	Q922q7 rattus norv	232	6	2.1	337	1	GCP SATV	P40731 salmonella
160	6	2.1	239	1	TRF8 MOUSE	Q35538 petromyzon	233	6	2.1	337	1	GPDA PASMU	Q9cl17 pasteurella
161	6	2.1	241	1	GLTL ECOLI	P32972 mus musculu	234	6	2.1	337	1	Z285 HUMAN	Q95218 homo sapien
162	6	2.1	242	1	CRP4 LIMPO	P10706 escherichia	235	6	2.1	338	1	FOSB MOUSE	P13346 mus musculu
163	6	2.1	243	1	TLP1 CASSA	Q9smh2 limulus pol	236	6	2.1	338	1	LUM HUMAN	P51884 homo sapien
164	6	2.1	243	1	ZIPA XANAC	Q9smh2 castanea sa	237	6	2.1	338	1	LUM MOUSE	P51885 mus musculu
165	6	2.1	244	1	FNRA PSEST	Q9pm10 xanthomonas	238	6	2.1	338	1	LUM RAT	P51886 rattus norv
166	6	2.1	244	1	ZIPA XANCP	P47200 pseudomonas	239	6	2.1	338	1	YEVY YEAST	P40093 saccharomyc
167	6	2.1	246	1	ATP6 CANPA	Q9pab7 xanthomonas	240	6	2.1	340	1	AA2B CHICK	O13076 gallus gall
168	6	2.1	248	1	1433 CAEBL	Q03671 candida par	241	6	2.1	340	1	ILVE HELPU	Q92jfi helicobacte
169	6	2.1	252	1	TI13 ARATH	P41932 caenorhabdi	242	6	2.1	340	1	ILVE HELPU	Q92jfi helicobacte
170	6	2.1	258	1	KDSB PASMU	O82598 arabidopsis	243	6	2.1	340	1	YK4P CAEBL	O26004 helicobacte
171	6	2.1	259	1	RNS2 ARATH	P57883 pasteurella	244	6	2.1	341	1	TA2R RAT	O17606 caenorhabdi
172	6	2.1	265	1	MPH1 HOLIA	P42814 arabidopsis	245	6	2.1	342	1	LUM BOVIN	P34978 rattus norv
173	6	2.1	266	1	YH42 CLOPE	P43216 holcus lana	246	6	2.1	343	1	TA2R CERAE	Q05443 bos taurus
174	6	2.1	267	1	DM1 YEAST	Q9xi17 clostridium	247	6	2.1	344	1	HYGH HYONI	P56486 cercopithe
175	6	2.1	268	1	CEBD MOUSE	P40200 saccharomyc	248	6	2.1	345	1	TRPD AERPE	P24397 hyoscyanus
176	6	2.1	268	1	CEBD RAT	Q00322 mus musculu	249	6	2.1	348	1	CTH2 MOUSE	Q9y8t2 aeropyrum p
177	6	2.1	269	1	YFCA ECOLI	P14008 escherichia	250	6	2.1	350	1	GANA ASPAC	Q9cyc5 mus musculu
178	6	2.1	274	1	CB2B PINSY	P15194 pinus sylve	251	6	2.1	351	1	B3AR CAVPO	P48842 apergillus
179	6	2.1	274	1	YB03 MYCTU	P71671 mycobacteri	252	6	2.1	353	1	CCPA ACEXY	Q60483 cavia porce

180	6	2.1	274	1	YX1 CVHSA	P59632 human coron
181	6	2.1	275	1	YMA9 CAEBL	P34454 caenorhabdi
182	6	2.1	280	1	PANB MYCVN	Q917b2 mycobacteri
183	6	2.1	281	1	PANB MYCTU	Q10505 mycobacteri
184	6	2.1	283	1	VNS4 MSTV	P33521 maize strip
185	6	2.1	284	1	DRN1 MOUSE	P43183 mus musculu
186	6	2.1	285	1	DDH2 HUMAN	Q95865 homo sapien
187	6	2.1	286	1	PANB MYCLE	Q9fhd5 arabidopsis
188	6	2.1	286	1	UDU1 ARATH	P34961 rice stripe
189	6	2.1	286	1	VNS4 RSMV	Q00847 rice stripe
190	6	2.1	286	1	VNS4 BSVT	P34961 rice stripe
191	6	2.1	289	1	BSN1 BACSU	Q03091 bacillus su
192	6	2.1	289	1	QCRC MYCLE	C69583 mycobacteri
193	6	2.1	292	1	U714 HUMAN	P50876 homo sapien
194	6	2.1	292	1	U714 MOUSE	Q925f3 mus musculu
195	6	2.1	294	1	CAMG MOUSE	P49070 mus musculu
196	6	2.1	296	1	CAMG HUMAN	P49069 homo sapien
197	6	2.1	299	1	CRX BOVIN	Q9xsk0 bos taurus
198	6	2.1	299	1	CRX HUMAN	O43186 homo sapien
199	6	2.1	299	1	CRX MOUSE	O54751 mus musculu
200	6	2.1	301	1	CTFS HUMAN	Q9uja2 homo sapien
201	6	2.1	303	1	CD38 RAT	Q64244 rattus norv
202	6	2.1	303	1	CTFS MOUSE	Q802m8 mus musculu
203	6	2.1	305	1	GSPC VIBCH	P45777 vibrio chol
204	6	2.1	306	1	PRVA ANASP	Q8yvt3 anabaena sp
205	6	2.1	306	1	YLIC SCOLI	P75798 escherichia
206	6	2.1	308	1	Y04F MYCTU	Q10786 mycobacteri
207	6	2.1	309	1	YQGH BACSU	P46339 bacillus su
208	6	2.1	311	1	FMT STRP6	Q8dmr7 streptococc
209	6	2.1	311	1	FMT STRP6	Q8dmr7 streptococc
210	6	2.1	311	1	YCAV CLOKL	P38943 clostridium
211	6	2.1	312	1	DRBX ANAPL	O57314 anas platyr
212	6	2.1	313	1	PRRB RHIME	Q92q15 rhizobium m
213	6	2.1	314	1	MER2 YEAST	P21651 saccharomyc
214	6	2.1	314	1	YP69 MYCTU	Q50652 mycobacteri
215	6	2.1	315	1	O3A2 HUMAN	P47893 homo sapien
216	6	2.1	318	1	MYOD RAT	Q02346 rattus norv
217	6	2.1	318	1	Y391 BUCBP	O89ac3 buchnera ap
218	6	2.1	319	1	CU06 HUMAN	P57060 homo sapien
219	6	2.1	320	1	YC55 PORPU	P51203 porphyra pu
220	6	2.1	322	1	FSA BRARE	Q99yva brachydanio
221	6	2.1	322	1	HEM3 CAUCR	Q9abz8 caulobacter
222	6	2.1	327	1	OPT CANFA	P33286 canis famli
223	6	2.1	330	1	PRC3 PORGI	P33437 porphyromon
224	6	2.1	331	1	LDHC HUMAN	P07864 homo sapien
225	6	2.1	334	1	PRC1 PORGI	P59916 porphyromon
226	6	2.1	335	1	DUSA SHEON	Q8aa10 shewanella
227	6	2.1	335	1	ZDH1 STAAM	Q99581 staphylococ
228	6	2.1	335	1	ZDH1 STAAM	Q8nvd1 staphylococ

253	1	353	1	CV04_MOUSE	Q8r5a6	mus musculus	326	6	2.1	422	1	GAS7_RAT	O55148	rattus norv
254	1	353	1	TCPH_TETH	P54410	tetrahymena	327	6	2.1	422	1	GSA_CHLTR	O84212	chlamydia t
255	1	355	1	TRPD_AZOB	P26924	azospirillum	328	6	2.1	424	1	HEMI_CHLVI	P28462	rhizobium
256	1	355	1	MURG_YERPE	Q8zie9	versinia pe	329	6	2.1	424	1	MSI3_ARATH	O22469	arabidopsis
257	1	356	1	SECV_BUCAK	P49976	buchnera ap	330	6	2.1	425	1	IFI5_MOUSE	Q08619	mus musculus
258	1	357	1	CADH_POPDE	P31657	populus del	331	6	2.1	425	1	PAR1_HUMAN	P25116	homo sapien
259	1	358	1	ILVE_STAAM	Q99w55	staphylococ	332	6	2.1	425	1	PAR1_FAPHA	P56488	papio namad
260	1	358	1	ILVE_STAEP	Q8c978	staphylococ	333	6	2.1	426	1	HEMI_RHOBA	Q7uk22	rhodospirell
261	1	360	1	CYS2_MAIZE	Q10717	zea mays (m	334	6	2.1	428	1	PAR1_CRILLO	Q00991	cricketulus
262	1	360	1	ELV2_MOUSE	Q60899	mus musculus	335	6	2.1	431	1	UL61_HCMWA	P16818	human cytom
263	1	360	1	YOPA_CABEL	Q09337	caenorhabdi	336	6	2.1	433	1	OADB_SLEPN	P13156	klebsiella
264	1	361	1	OPCT_BOVIN	Q28120	bos taurus	337	6	2.1	433	1	OADB_KALPT	Q829m6	salmonella
265	1	362	1	ILVE_STRGO	Q86585	streptomyce	338	6	2.1	435	1	OADB_HAEDU	Q9-f98	haemophilus
266	1	364	1	FTSW_BORBU	Q44775	borrelia bu	339	6	2.1	436	1	SH6_RAT	P31388	rattus norv
267	1	364	1	UFTG_PEA	O04300	pisum sativ	340	6	2.1	436	1	MUAI_BACSU	P70965	bacillus su
268	1	365	1	BCSA_BACSU	P54157	bachillus su	341	6	2.1	438	1	MUAI_LACPL	Q88uu5	lactobacill
269	1	365	1	MAP3_SCHPO	P31397	schizosacch	342	6	2.1	438	1	PROA_ANASP	Q8yv15	anabaena sp
270	1	368	1	ILVE_MYCLE	Q32954	mycobacteri	343	6	2.1	440	1	SH6_HUMAN	P50406	homo sapien
271	1	368	1	ILVE_MYCTU	Q10398	mycobacteri	344	6	2.1	440	1	SH6_MOUSE	Q9r1c8	mus musculus
272	1	369	1	TA2R_HUMAN	P21731	homo sapien	345	6	2.1	441	1	DTA2_RHIME	P20672	rhizobium m
273	1	372	1	AOB_PFROM	Q9v781	prochloroco	346	6	2.1	442	1	DTA2_RHILO	Q986r8	rhizobium l
274	1	372	1	S17B_HUMAN	Q94768	homo sapien	347	6	2.1	443	1	YABL_HAEIN	P44936	haemophilus
275	1	373	1	MLE_TRICU	P46057	trichosporo	348	6	2.1	444	1	DTA2_RHILE	Q01857	rhizobium l
276	1	376	1	MYG1_HUMAN	Q9hb07	homo sapien	349	6	2.1	444	1	LH2A_MOUSE	Q99kx8	mus musculus
277	1	376	1	N1FV_AZOB	P70728	azospirillum	350	6	2.1	445	1	EM47_YEAST	P43555	saccharomyc
278	1	376	1	N1FV_ANASP	P58637	anabaena sp	351	6	2.1	445	1	MEJ3_BUCAP	Q8ka23	buchnera ap
279	1	377	1	NORW_SALTI	Q824c4	salmonella	352	6	2.1	446	1	GRWD_HUMAN	Q9bq67	homo sapien
280	1	377	1	PEPC_MACFU	Q8zmj6	macaca fusc	353	6	2.1	448	1	DTA2_AGRTS	P58r34	agrobacteri
281	1	377	1	PEPC_MACFU	P03955	macaca fusc	354	6	2.1	451	1	NORM_DEIRA	Q9ry44	deinococcus
282	1	380	1	MYG1_MOUSE	Q3j5k1	mus musculus	355	6	2.1	451	1	VNUC_THOYG	P89216	thogoto vir
283	1	381	1	E2BB_YEAST	P32502	saccharomyc	356	6	2.1	454	1	C6ST_CHICK	Q92179	gallus gall
284	1	381	1	PPAP_RAT	P20646	rattus norv	357	6	2.1	460	1	LE12_SULTO	Q971s5	sulfolobus
285	1	381	1	SSUD_PSEAE	Q3hy32	pseudomonas	358	6	2.1	461	1	DTA2_RHIGA	Q9x7k6	rhizobium g
286	1	382	1	N1FV_AZOBH	P23122	azotobacter	359	6	2.1	463	1	RBL3_HYDMR	Q59462	hydrogenovi
287	1	382	1	SSUD_BUTSP	Q9khr3	butiauxell	360	6	2.1	465	1	TPSN_MOUSE	Q9r233	mus musculus
288	1	382	1	SSUD_PSEPK	Q88r95	pseudomonas	361	6	2.1	465	1	VATB_PYRAB	Q9uxu8	pyrococcus
289	1	382	1	SSUD_PSEPU	O85764	pseudomonas	362	6	2.1	465	1	VATB_PYRHO	O57729	pyrococcus
290	1	382	1	SSUD_PSESP	Q8khs2	pseudomonas	363	6	2.1	470	1	PROP_CAVPO	Q64181	cavia porce
291	1	382	1	SSUD_YERPE	Q8zb04	versinia pe	364	6	2.1	471	1	ATPA_PROMO	P29706	propionigen
292	1	384	1	OXA4_YSNY3	P74155	synecocyst	365	6	2.1	473	1	SYC_METMA	Q89vq1	methanosarc
293	1	385	1	N1FV_AZOV1	P05342	azotobacter	366	6	2.1	475	1	SYC_CHLMU	Q9ple0	chlamydia m
294	1	387	1	COAT_TBSVB	P11795	tomato bush	367	6	2.1	477	1	DTA1_RHILO	Q98av2	rhizobium l
295	1	388	1	PEPC_CALJA	Q9n2d3	callithrix	368	6	2.1	477	1	P3_HUMAN	P09131	homo sapien
296	1	388	1	PEPC_HUMAN	P20142	homo sapien	369	6	2.1	479	1	B3GP_DROME	Q9vrtg7	drosophila
297	1	388	1	TRA6_BURCE	P24575	burkholderi	370	6	2.1	479	1	GLYC_NEUCR	P34898	neurospora
298	1	388	1	YF02_AQUAE	O57472	aquifex aeo	371	6	2.1	483	1	PREG_NEUCR	Q06712	neurospora
299	1	389	1	GSPL_AERRY	P45789	aeromonas h	372	6	2.1	485	1	ALGI_PSEPK	Q88nd2	pseudomonas
300	1	390	1	ISDF_BRUME	Q5yhd8	b ispd/ispf	373	6	2.1	485	1	GATA_CLOTE	Q89iil	clostridium
301	1	390	1	ISDF_BRUSU	Q8g0h4	b ispd/ispf	374	6	2.1	485	1	NOE1_HUMAN	Q99784	homo sapien
302	1	390	1	NCF1_HUMAN	P14598	homo sapien	375	6	2.1	485	1	NOE1_MOUSE	O88998	mus musculus
303	1	390	1	SUCC_COXBU	P33592	coxiella bu	376	6	2.1	485	1	PODX_RAT	Q62609	rattus norv
304	1	392	1	CMLR_STRLI	P31141	streptomyce	377	6	2.1	485	1	PODX_RAT	Q9wtq2	rattus norv
305	1	392	1	MP14_AMBAR	P28744	ambrosia ar	378	6	2.1	487	1	HEP_DROME	Q23977	drosophila
306	1	396	1	HEMI_CLOBP	Q97mu6	clostridium	379	6	2.1	488	1	ZDHE_HUMAN	Q81zn3	homo sapien
307	1	400	1	HEPK_VIBPA	P40605	vibrio para	380	6	2.1	490	1	C71L_ARATH	Q98c12	arabidopsis
308	1	403	1	GBA8_DICDI	P34046	dictyosteli	381	6	2.1	490	1	C71M_ARATH	Q98atl1	arabidopsis
309	1	404	1	NEED_PINRA	O04407	pinus radia	382	6	2.1	490	1	C72F_ARATH	Q91w27	arabidopsis
310	1	408	1	YL12_PYRAE	Q8zv99	pyrobaculum	383	6	2.1	490	1	ENGA_CHLMU	Q9plm3	chlamydia m
311	1	409	1	CP52_STRCC	Q59831	streptomyce	384	6	2.1	490	1	ENGA_CHLTR	O84709	chlamydia t
312	1	411	1	LCYB_SYNP7	Q55276	synecococc	385	6	2.1	494	1	CPA4_MOUSE	P15392	mus musculus
313	1	414	1	PLT_MYCLE	Q50173	mycobacteri	386	6	2.1	494	1	CPA5_MOUSE	P20852	mus musculus
314	1	414	1	SYC2_MYCTU	Q33264	mycobacteri	387	6	2.1	494	1	HEX3_ADEMI	O10438	mouse adeno
315	1	414	1	YOJL_BACSU	Q31852	bacillus su	388	6	2.1	496	1	DHAL_CLAHE	P40108	cladosporiu
316	1	416	1	MYTK_SYNEL	Q8dk88	synecococc	389	6	2.1	497	1	CV04_MACFA	Q95k11	macaca fasc
317	1	417	1	IF_MOUSE	P52787	mus musculus	390	6	2.1	497	1	GALT_ENTFA	Q836n8	enterococcu
318	1	419	1	PKK2_CAEHL	Q8mx14	caenorhabdi	391	6	2.1	497	1	HMES_DROME	P18488	drosophila
319	1	421	1	GAS7_MOUSE	Q60780	mus musculus	392	6	2.1	497	1	IRF5_MOUSE	P56477	mus musculus
320	1	421	1	SP39_BRUBA	O06875	brucella ab	393	6	2.1	498	1	IRF5_MOUSE	P31473	escherichia
321	1	421	1	SP39_BRUME	Q8yce2	brucella me	394	6	2.1	499	1	YIEN_SCOLI	Q8mey4	ceratozamia
322	1	421	1	SP39_BRUSU	Q8fvx5	brucella su	395	6	2.1	499	1	MATK_CERME	Q01870	penicillium
323	1	421	1	SVTC_HUMAN	Q8iv01	homo sapien	396	6	2.1	500	1	C72W_ARATH	Q91lp5	arabidopsis
324	1	421	1	SVTC_MOUSE	Q920n7	mus musculus	397	6	2.1	502	1	ACH7_CHICK	P22770	gallus gall
325	1	421	1	SVTC_RAT	P97610	rattus norv	398	6	2.1	502	1	ACH7_HUMAN	P36544	homo sapien

399	6	2.1	502	1	SVK_HAEIN	P43825	haemophilus	472	6	2.1	624	1	P212_HUMAN	Q9hzm6	homo sapien
400	6	2.1	502	1	Y2R2_AGRVI	P70795	agrobacteri	473	6	2.1	625	1	FANA_HELAS	Q25011	helix asper
401	6	2.1	503	1	PODX_MOUSE	Q9r0m4	mus musculus	474	6	2.1	626	1	EXON_HSV11	P04294	herpes simp
402	6	2.1	503	1	STE_CHLTE	Q5f724	chlorobium	475	6	2.1	626	1	HCYB_SURCA	Q9afh9	eurytelma c
403	6	2.1	504	1	PUPP_HAEIN	P45174	haemophilus	476	6	2.1	626	1	PRIM_LISIN	Q92bq5	listeria in
404	6	2.1	504	1	YBLH_SCHPO	Q10341	schizosacch	477	6	2.1	627	1	THIC_FSEPK	Q88da5	pseudomonas
405	6	2.1	506	1	ALG6_SCHPO	Q43053	schizosacch	478	6	2.1	627	1	Y1L6_PANTR	Q43296	homo sapien
406	6	2.1	506	1	C992_ARATH	Q42602	arabidopsis	479	6	2.1	631	1	YL16_PANTR	O62666	pan troglod
407	6	2.1	508	1	CG12_HUMAN	Q96kn2	homo sapien	480	6	2.1	638	1	YCSB_SCHPO	Q74910	schizosacch
408	6	2.1	511	1	INO1_PHAVU	Q41107	phasolus v	481	6	2.1	639	1	XNG_RAT	P08934	rattus norv
409	6	2.1	516	1	OXLA_CROAD	Q93364	crotalus ad	482	6	2.1	640	1	DXS_CAUCR	Q9aem5	caulobacter
410	6	2.1	516	1	YLAB_ECOLI	P77473	escherichia	483	6	2.1	640	1	IP14_MOUSE	P15092	mus musculus
411	6	2.1	517	1	CPN1_RANCA	Q92104	rana catesb	484	6	2.1	645	1	SUBB_BACSU	P16396	bacillus su
412	6	2.1	517	1	CV04_HUMAN	Q8wua7	homo sapien	485	6	2.1	645	1	Y081_CABEL	P34617	caenorhabdi
413	6	2.1	521	1	COAT_BPT4	P04535	bacterioph	486	6	2.1	647	1	PARE_STRPN	Q59961	streptococ
414	6	2.1	524	1	GAPD_SYNP7	P29686	synecococ	487	6	2.1	652	1	NAK1_SCHPO	O75011	schizosacch
415	6	2.1	524	1	Y833_SYNP3	P74217	synecocyst	488	6	2.1	657	1	CTPD_MYCTU	O53160	mycobacteri
416	6	2.1	526	1	4P2_MOUSE	P10852	mus musculus	489	6	2.1	670	1	ACL1_NEUCR	Q8X097	neurospora
417	6	2.1	527	1	TCPD_SCHPO	P50999	schizosacch	490	6	2.1	673	1	Z145_HUMAN	Q05516	homo sapien
418	6	2.1	528	1	PODX_HUMAN	Q00592	homo sapien	491	6	2.1	679	1	NADE_MYCTU	P71911	mycobacteri
419	6	2.1	528	1	WR42_ARATH	Q9xec3	arabidopsis	492	6	2.1	680	1	NADE_MYCTU	Q9cbz6	mycobacteri
420	6	2.1	529	1	4P2_HUMAN	P08195	homo sapien	493	6	2.1	685	1	DL14_HUMAN	Q09r61	homo sapien
421	6	2.1	529	1	YP77_MYCTU	Q50644	mycobacteri	494	6	2.1	687	1	V1UA_VIBCH	Q00964	vibrio chol
422	6	2.1	532	1	YOAD_ECOLI	P76261	escherichia	495	6	2.1	699	1	EPG_AQUAE	O66428	aquifex aeo
423	6	2.1	533	1	YF03_MYCTU	Q97222	mycobacteri	496	6	2.1	699	1	EPG_AQUAE	P46211	aquifex pyr
424	6	2.1	536	1	OXAA_WOLSU	Q97161	clostridium	497	6	2.1	702	1	OPGB_XANCP	Q8pdd7	xanthomonas
425	6	2.1	536	1	OXAA_WOLSU	P60037	wolinetella s	498	6	2.1	703	1	CANX_MOUSE	Q8bnd6	mus musculus
426	6	2.1	537	1	PYRG_RICCN	Q92197	rickettsia	499	6	2.1	705	1	CANX_CHICK	P00789	gallus gall
427	6	2.1	537	1	TVR1_MOUSE	P07147	mus musculus	500	6	2.1	705	1	MMLC_STRCO	O88022	streptomyce
428	6	2.1	538	1	GLE1_YEAST	Q12315	saccharomyc	501	6	2.1	705	1	MMLC_STRCO	Q9xa86	streptomyce
429	6	2.1	538	1	WR31_ARATH	Q93wto	arabidopsis	502	6	2.1	705	1	YNP9_CAEEL	P34562	caenorhabdi
430	6	2.1	540	1	OXAA_WIGER	Q8d318	wiggleswort	503	6	2.1	706	1	EPG_LBPIN	Q8f983	leptospi
431	6	2.1	544	1	OXAA_BORBU	O51398	borrelia bu	504	6	2.1	707	1	CNAI_HUMAN	Q9nx78	homo sapien
432	6	2.1	545	1	MR9_MOUSE	Q922d0	mus musculus	505	6	2.1	710	1	NECB_HYDAT	P29145	hydra atten
433	6	2.1	546	1	PHR2_CANAL	Q13318	cardia alb	506	6	2.1	711	1	LXE3_HUMAN	Q9pyj1	homo sapien
434	6	2.1	548	1	CH60_EHRSI	P48214	ehrllichia r	507	6	2.1	711	1	LXE3_MOUSE	Q9wv07	mus musculus
435	6	2.1	548	1	CH60_EHRSI	Q32606	ehrllichia r	508	6	2.1	713	1	CAN1_MOUSE	Q53550	mus musculus
436	6	2.1	549	1	MR9_HUMAN	Q96gg7	homo sapien	509	6	2.1	713	1	CAN1_RAT	P97571	rattus norv
437	6	2.1	551	1	CC14_YEAST	Q00684	saccharomyc	510	6	2.1	713	1	PRVL_BRARE	Q9w757	brachydanio
438	6	2.1	551	1	L1DP_ECOL6	Q8xd99	escherichia	511	6	2.1	713	1	YKX1_YEAST	P50944	saccharomyc
439	6	2.1	551	1	L1DP_ECOLI	P33231	escherichia	512	6	2.1	714	1	CAN1_HUMAN	P50944	saccharomyc
440	6	2.1	551	1	PODX_RABIT	Q28645	cryptolagus	513	6	2.1	714	1	CAN1_MACFA	Q07384	homo sapien
441	6	2.1	552	1	HAS2_CHICK	O57424	gallus gall	514	6	2.1	722	1	CAN1_PIG	Q95192	macaca faec
442	6	2.1	552	1	Y932_METJA	Q58688	methanococ	515	6	2.1	722	1	FLID_TREPA	O83842	treponema p
443	6	2.1	555	1	ALG9_YEAST	P53868	saccharomyc	516	6	2.1	725	1	CTPC_MYCLE	Q9Gc11	mycobacteri
444	6	2.1	557	1	LYPB_SERVA	P53321	seriatia ma	517	6	2.1	726	1	RNR_MYCPN	P75529	mycoplasma
445	6	2.1	558	1	THPB_TETPY	P54409	tetrahymena	518	6	2.1	728	1	MYBA_XENLA	Q05935	xenopus lae
446	6	2.1	560	1	YDEN_ECOLI	P77318	escherichia	519	6	2.1	739	1	PO21_CHICK	P15143	gallus gall
447	6	2.1	563	1	MDL1_PRUSE	P62706	prunus sero	520	6	2.1	741	1	RNSA_HUMAN	Q05823	homo sapien
448	6	2.1	566	1	MXID_SHIFL	Q04641	shigella fl	521	6	2.1	741	1	TKTC_SOLTU	Q43848	solanum tub
449	6	2.1	566	1	MXID_SHISO	Q52933	shigella so	522	6	2.1	743	1	PO21_HUMAN	P14859	homo sapien
450	6	2.1	570	1	FLIP_RHOSH	Q53151	rhodobacter	523	6	2.1	744	1	HXG1_HABIN	P44523	haemophilus
451	6	2.1	573	1	MDL3_PRUSE	P62707	prunus sero	524	6	2.1	745	1	PO21_PIG	Q29076	sus scrofa
452	6	2.1	574	1	GAGJ_DROFU	P21331	drosophila	525	6	2.1	747	1	ORPB_HUMAN	Q9bxb4	homo sapien
453	6	2.1	575	1	UL87_EBV	P52515	epstein-bar	526	6	2.1	749	1	CATA_LEGPN	Q09xb9	legionella
454	6	2.1	577	1	YGSU_YEAST	P53333	saccharomyc	527	6	2.1	753	1	YP6A_CABEL	Q09219	caenorhabdi
455	6	2.1	580	1	CPXA_PSESM	Q87vb6	pseudomonas	528	6	2.1	758	1	PARC_RHIME	Q59749	rhizobium m
456	6	2.1	580	1	PREX_BACCR	Q81cb2	bacillus ce	529	6	2.1	759	1	PURL_CHLTE	Q8kd17	chlorobium
457	6	2.1	581	1	YH2_YEAST	P38767	saccharomyc	530	6	2.1	760	1	PO21_XENLA	P16143	xenopus lae
458	6	2.1	583	1	TREA_HUMAN	Q43280	homo sapien	531	6	2.1	763	1	GLH1_CAEEL	P34689	caenorhabdi
459	6	2.1	593	1	SUMT_YEAST	P36150	saccharomyc	532	6	2.1	770	1	PO21_MOUSE	P25425	mus musculus
460	6	2.1	594	1	DCF2_SCHPO	Q92345	schizosacch	533	6	2.1	775	1	POQF_PSEAE	Q912d2	pseudomonas
461	6	2.1	601	1	KEFB_SALT1	Q821y7	salmonella	534	6	2.1	777	1	RTN1_RAT	Q64548	rattus norv
462	6	2.1	601	1	KEFB_SALT1	Q821l3	salmonella	535	6	2.1	780	1	A4_TETFL	O73683	tetradon f
463	6	2.1	606	1	T9S1_HUMAN	O15321	homo sapien	536	6	2.1	781	1	YK37_CAEEL	P46557	caenorhabdi
464	6	2.1	606	1	T9S1_MOUSE	Q8dbu0	mus musculus	537	6	2.1	781	1	PUR2_YARLI	Q99148	y bifunctio
465	6	2.1	608	1	GLMS_BUCAL	P57138	b glucosami	538	6	2.1	790	1	SEIL_MOUSE	Q92296	mus musculus
466	6	2.1	609	1	FRI_ARATH	Q9fdw0	arabidopsis	539	6	2.1	793	1	NECA_HYDAT	P29146	hydra atten
467	6	2.1	616	1	YK44_CAEEL	P34256	caenorhabdi	540	6	2.1	805	1	SUS1_SOLTU	P10691	solanum tub
468	6	2.1	620	1	DNAA_PORPU	P30723	porphyra pu	541	6	2.1	805	1	SUS2_SOLTU	P49039	solanum tub
469	6	2.1	620	1	UL32_HSVB	P28952	equine herp	542	6	2.1	805	1	SUSY_LYCES	P49037	lycopersico
470	6	2.1	622	1	CN31_HUMAN	Q96ne9	homo sapien	543	6	2.1	808	1	DHG_GLUOX	P27175	gluconobact
471	6	2.1	623	1	ZPL_MOUSE	Q62005	mus musculus	544	6	2.1	809	1	AL14_SCHPO	Q94534	schizosacch

691	6	2.1	3432	1	POLG_JAEVJ	P32886	j genome po	764	1.7	70	1	GVPA_MICBC	P08412	microcystis
692	6	2.1	3433	1	POLG_KUNJM	P14335	k genome po	765	1.7	70	1	PRRH_THERH	P43891	thermus the
693	6	2.1	3588	1	SRF1_BACSU	P27206	bacillus su	766	1.7	71	1	RNZA_RANPI	Q8dfq3	rana pipien
694	6	2.1	3803	1	TRAI1_DROME	Q818u7	drosophila	767	1.7	70	1	CKOA_CONMA	P05484	cnus magus
695	6	2.1	4289	1	DNKC_NEUCR	P22105	homo sapien	768	1.7	71	1	FTSB_BUCAT	P57496	buchnera ap
696	6	2.1	4367	1	TYXK_NEUCR	P45443	neurospora	769	1.7	71	1	GVPA_PLAAG	Q9r3v0	planktothri
697	6	2.1	4655	1	LAP2_HUMAN	P98164	homo sapien	770	1.7	71	1	GVPA_PSEAN	P22453	pseudanaba
698	6	2.1	4829	1	BR16_HUMAN	Q9nr09	homo sapien	771	1.7	71	1	YORN_TTV1	P19298	thermoprote
699	6	2.1	5147	1	PCLO_HUMAN	Q9y6v0	homo sapien	772	1.7	72	1	CKX7_CONPU	P56533	cnus purpu
700	6	2.1	8797	1	SNE1_HUMAN	Q9nf91	homo sapien	773	1.7	72	1	GBC_SCHPO	O94309	schizosach
701	7	1.7	20	1	JHPB_PAPSP	P80055	papio sp. (774	1.7	72	1	HSUJ_BUCSC	O63227	buchnera ap
702	5	1.7	20	1	YX6B_ODOSI	P41627	bombyx mori	775	1.7	72	1	LR18_RHOTE	P80588	rhodocyclu
703	5	1.7	26	1	YX6B_ODOSI	P49832	odontella s	776	1.7	72	1	RR18_ODOSI	P49505	odontella s
704	5	1.7	28	1	CH60_MYCSM	P80673	mycobacteri	777	1.7	72	1	VPI3_BPPH6	P11130	bacterioph
705	5	1.7	29	1	ATPA_ERYNA	P26965	bryopsis ma	778	1.7	73	1	VPB_Bp186	P08711	bacterioph
706	5	1.7	29	1	H2B2_ECHES	P13282	echinus esc	779	1.7	74	1	IFI_FUSNN	Q8r5w2	fusobacteri
707	5	1.7	29	1	SODC_OLEEU	P80740	olea europ	780	1.7	74	1	DR35_PEA	Q01784	pisum sativ
708	5	1.7	30	1	END2_ONCKE	P01205	oncorhynch	781	1.7	74	1	EDDF_HUMAN	O60584	homo sapien
709	5	1.7	30	1	TL16_SPIOL	P18134	spinacia ol	782	1.7	74	1	SRP_SOYBN	Q07502	glycine max
710	5	1.7	31	1	Y3KD_BPCBP	P19187	bacterioph	783	1.7	74	1	WDNM_RAT	P14730	rattus norv
711	5	1.7	32	1	MDH_NITAL	P10887	nitroschias	784	1.7	75	1	YDCE_ECO57	Q8x9x8	escherichia
712	5	1.7	36	1	PSAI_ANGLY	P28251	angiopteris	785	1.7	75	1	YV96_ANASP	Q8y9s5	anabaena sp
713	5	1.7	36	1	PSAI_MARPO	P12185	marchantia	786	1.7	76	1	SIRA_BUCAT	P57522	buchnera ap
714	5	1.7	36	1	PSAI_PSIUN	Q8w110	psilotum nu	787	1.7	76	1	YDCE_ECOLI	P31992	escherichia
715	5	1.7	37	1	PTGT_PORPU	P51318	porphyra pu	788	1.7	77	1	VG68_BFMD2	O64260	mycobacteri
716	5	1.7	37	1	V11_BPF2	P19347	bacterioph	789	1.7	77	1	YOCN_BACSU	O34855	bacillus su
717	5	1.7	38	1	PSEY_CYPAP	P48272	cyanophora	790	1.7	78	1	RUB3_ARATH	O65381	arabidopsal
718	5	1.7	38	1	TXMI_MACGS	P33557	macrothale	791	1.7	78	1	VG9_SPV1R	P15900	spiropasma
719	5	1.7	39	1	COLI_STRCA	P01196	struthio ca	792	1.7	78	1	Y009_BPL2	P42544	bacterioph
720	5	1.7	39	1	P8BL_SYNY3	Q55354	synechocyst	793	1.7	79	1	CSMA_CHLAU	P09928	chloroflexu
721	5	1.7	40	1	H2B3_ECHES	P13283	echinus esc	794	1.7	79	1	YKSF_ECOLI	P75677	escherichia
722	5	1.7	44	1	PHRA_BACSU	Q00829	bacillus su	795	1.7	79	1	Y222_METJA	Q60259	methanococ
723	5	1.7	44	1	RIP3_WOMCH	P24817	momordica c	796	1.7	80	1	LYNX_HUMAN	Q9bz99	homo sapien
724	5	1.7	44	1	V85_FAPVR	P21403	reindeer pa	797	1.7	81	1	NUML_HUMAN	O00483	homo sapien
725	5	1.7	46	1	RPOF_METJA	P59283	methanococ	798	1.7	81	1	Y791_TREPA	Q83770	treponema p
726	5	1.7	49	1	Y195_EPT7	P03804	bacterioph	799	1.7	82	1	Y070_METJA	Q60373	methanococ
727	5	1.7	50	1	ATPE_BOVIN	P05632	bos taurus	800	1.7	82	1	YH19_STRMU	Q8dsg4	streptococ
728	5	1.7	50	1	ATPE_HUMAN	P56381	homo sapien	801	1.7	82	1	Y182_STRPN	Q97nx1	streptococ
729	5	1.7	51	1	ATPE_MOUSE	P56382	mus musculu	802	1.7	83	1	BLE2_STAAN	P24491	staphylococ
730	5	1.7	52	1	PH68_HUMAN	Q9uht9	homo sapien	803	1.7	83	1	DLX2_RAT	Q64204	rattus norv
731	5	1.7	52	1	V88_EPV4	P08352	bovine sapi	804	1.7	83	1	DPM2_MOUSE	Q92324	mus musculu
732	5	1.7	53	1	LECI_LATOC	P23306	lathyrus oc	805	1.7	84	1	ACP_EORPU	Q92325	rattus norv
733	5	1.7	53	1	LECA_LATAR	P07442	lathyrus ar	806	1.7	84	1	Y076_NPVAC	P51280	porphyra pu
734	5	1.7	54	1	RK32_TOBAC	P12198	nicotiana t	807	1.7	84	1	Y076_NPVAC	Q06690	autographa
735	5	1.7	55	1	ELA6_ADE05	P24934	human adeno	808	1.7	85	1	CYB_FONNI	O10329	oryzia psu
736	5	1.7	55	1	ELA6_ADE05	P06438	human adeno	809	1.7	85	1	CYB_FONNI	P29670	pomoxia nig
737	5	1.7	56	1	VGG_BPHX	P03653	bacterioph	810	1.7	85	1	FCBG_BOVIN	Q9bdr7	bos taurus
738	5	1.7	58	1	COX1_CAPHI	Q36347	capra hircu	811	1.7	85	1	SIX2_BUTJU	P24336	buthotus ju
739	5	1.7	59	1	SKA_LEIGH	P13487	leirus qui	812	1.7	85	1	THIO_METJA	Q57755	methanococ
740	5	1.7	59	1	SKB_LEIGH	P59943	leirus qui	813	1.7	85	1	FCBG_CAVPO	Q07249	cavia porce
741	5	1.7	59	1	SKD_LEIGH	P45628	leirus qui	814	1.7	86	1	FCBG_HUMAN	P30273	homo sapien
742	5	1.7	59	1	YAM5_CABEL	Q17638	caenorhabdi	815	1.7	86	1	FCBG_MOUSE	P20491	mus musculu
743	5	1.7	60	1	Y787_RICPR	O05977	rickettsia	816	1.7	86	1	FCBG_PIG	Q9xsz6	mus scrofa
744	5	1.7	62	1	GVPA_OSCAG	P80996	oscillatori	817	1.7	86	1	FCBG_RAT	P20411	rattus norv
745	5	1.7	62	1	YX65_GUTH	O78459	guillardia	818	1.7	86	1	RL23_METVA	P10143	methanococ
746	5	1.7	63	1	Y116_RICCN	Q92jff	rickettsia	819	1.7	86	1	TRL_HELPY	O87326	helicobacte
747	5	1.7	64	1	VG24_BPMU	Q9ctx0	bacterioph	820	1.7	86	1	YABO_BACSU	P37557	bacillus su
748	5	1.7	65	1	Y234_BACHD	Q9kg78	bacillus ha	821	1.7	86	1	YB1J_ECOLI	P41038	escherichia
749	5	1.7	66	1	FTSB_BUCAP	O8k9d5	buchnera ap	822	1.7	87	1	NDOA_PSEFL	Q45974	caulobacter
750	5	1.7	66	1	GVPA_AMOPE	P80998	ameobacte	823	1.7	87	1	YR54_SYNY3	O07823	pseudomonas
751	5	1.7	66	1	RPON_VYRAE	O8zyp9	pyrobaculum	824	1.7	87	1	YR54_SYNY3	P41464	autographa
752	5	1.7	67	1	Y136_VIBVU	Q8zbi1	vibrio vuln	825	1.7	88	1	YR54_SYNY3	P58235	synechocyst
753	5	1.7	67	1	YJBS_ECOLI	P58036	escherichia	826	1.7	88	1	YR54_SYNY3	O69250	bacillus me
754	5	1.7	67	1	YP74_VIBVY	Q7mies	vibrio vuln	827	1.7	88	1	YR54_SYNY3	P12552	bacterioph
755	5	1.7	68	1	BD01_HUMAN	P60022	homo sapien	828	1.7	88	1	YK9_BPP4	O28466	archaeoglob
756	5	1.7	68	1	BD01_NACMU	O18794	macaca mula	829	1.7	88	1	YK9_BPP4	Q28053	archaeoglob
757	5	1.7	68	1	BD01_PANTR	P60023	pan troglod	830	1.7	89	1	YK9_BPP4	P33134	escherichia
758	5	1.7	68	1	Y415_ARCFU	O29832	archaeoglob	831	1.7	89	1	FLIQ_ECOLI	P54701	salmonella
759	5	1.7	68	1	Y415_VIBPA	O87mc1	vibrio para	832	1.7	89	1	FLIQ_SALTY	O32967	mycobacteri
760	5	1.7	69	1	VC_RABVA	P15201	rabies viru	833	1.7	89	1	RS15_MYCLE	O33327	mycobacteri
761	5	1.7	70	1	GVPA_ANAFL	P10397	anabaena fl	834	1.7	90	1	YK9_BPP4	P51921	pagrus majo
762	5	1.7	70	1	GVPA_ANASP	Q8x9f1	anabaena sp	835	1.7	90	1	YK9_BPP4	P51923	sparus aua
763	5	1.7	70	1	GVPA_FREDI	P07060	fremyella d	836	1.7	91	1	NULN_BRALA	O79420	branchiosto

837	5	1.7	91	1	RK23	MARPO	P06390	marchantia	910	5	1.7	103	1	NDOA	PSEAE	Q51493	pseudomonas
838	5	1.7	91	1	VE5A	HPV11	P04017	human papil	911	5	1.7	103	1	NDOA	PSEPU	P23082	pseudomonas
839	5	1.7	91	1	VE5A	HPV6A	Q84296	human papil	912	5	1.7	103	1	OST4	PIG	Q2381	sus scrofa
840	5	1.7	91	1	VE5A	HPV6B	P06460	human papil	913	5	1.7	103	1	PHS	CHICK	Q73930	g.ptein-4-
841	5	1.7	91	1	VE5A	HPV6C	P20970	human papil	914	5	1.7	103	1	SPGB	HUMAN	Q8648	homo sapien
842	5	1.7	91	1	GONI	CHICK	P37042	gallus gall	915	5	1.7	103	1	SPGB	PANTR	Q9mz28	pan troglod
843	5	1.7	92	1	K11B	LEIN	Q25297	leishmania	916	5	1.7	103	1	GRO	CAVPO	O28815	archaeoglob
844	5	1.7	92	1	K11C	LEIN	Q25298	leishmania	917	5	1.7	103	1	GRO	CAVPO	O55235	cavia porce
845	5	1.7	92	1	KM11	LEIDO	Q26736	leishmania	918	5	1.7	104	1	PAPB	ECOLI	P04744	saccharomy
846	5	1.7	92	1	KM11	LEITR	Q21436	leishmania	919	5	1.7	104	1	YNS3	YEAST	P51828	saccharomy
847	5	1.7	92	1	POOD	XANCP	Q8p6m8	xanthomonas	920	5	1.7	105	1	INS	ONCKE	P51828	saccharomy
848	5	1.7	92	1	YK04	RABIT	P46632	oryctolagus	921	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
849	5	1.7	92	1	YK04	RABIT	P46632	oryctolagus	922	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
850	5	1.7	92	1	YK04	RABIT	P46632	oryctolagus	923	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
851	5	1.7	93	1	YK04	RABIT	P46632	oryctolagus	924	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
852	5	1.7	93	1	YK04	RABIT	P46632	oryctolagus	925	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
853	5	1.7	94	1	YK04	RABIT	P46632	oryctolagus	926	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
854	5	1.7	94	1	YK04	RABIT	P46632	oryctolagus	927	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
855	5	1.7	95	1	YK04	RABIT	P46632	oryctolagus	928	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
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862	5	1.7	96	1	YK04	RABIT	P46632	oryctolagus	935	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
863	5	1.7	96	1	YK04	RABIT	P46632	oryctolagus	936	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
864	5	1.7	96	1	YK04	RABIT	P46632	oryctolagus	937	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
865	5	1.7	96	1	YK04	RABIT	P46632	oryctolagus	938	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
866	5	1.7	97	1	YK04	RABIT	P46632	oryctolagus	939	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
867	5	1.7	97	1	YK04	RABIT	P46632	oryctolagus	940	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
868	5	1.7	97	1	YK04	RABIT	P46632	oryctolagus	941	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
869	5	1.7	98	1	YK04	RABIT	P46632	oryctolagus	942	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
870	5	1.7	98	1	YK04	RABIT	P46632	oryctolagus	943	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
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872	5	1.7	98	1	YK04	RABIT	P46632	oryctolagus	945	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
873	5	1.7	98	1	YK04	RABIT	P46632	oryctolagus	946	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
874	5	1.7	98	1	YK04	RABIT	P46632	oryctolagus	947	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
875	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	948	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
876	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	949	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
877	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	950	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
878	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	951	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
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887	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	960	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
888	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	961	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
889	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	962	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
890	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	963	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
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905	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	978	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
906	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	979	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
907	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	980	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
908	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	981	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph
909	5	1.7	99	1	YK04	RABIT	P46632	oryctolagus	982	5	1.7	105	1	YNS3	YEAST	P08387	bacterioph

883 5 1.7 115 1 Y341_NEIMA Q9jwjb neisseria m
 884 5 1.7 115 1 YC83_MYCPN P75494 mycoplasma
 885 5 1.7 115 1 YK89_NEIME Q9jxe2 neisseria m
 886 5 1.7 116 1 FRD2_PASMU Q9cp59 pasteurella
 887 5 1.7 116 1 GUAN_MOUSE P33680 mus musculus
 888 5 1.7 116 1 NU3M_STRCA Q79102 struchio ca
 889 5 1.7 116 1 PAND_LEPIN Q8cve3 leptospira
 890 5 1.7 116 1 Y784_METUA Q58174 methanococc
 891 5 1.7 117 1 HCT1_CHLPS Q46204 chlamydia p
 892 5 1.7 117 1 RL18_BUCAK P46182 buchnera ap
 893 5 1.7 117 1 RL18_ECOLI P02419 escherichia
 894 5 1.7 117 1 V13K_TRVPL P33776 tobacco rat
 895 5 1.7 117 1 V13K_BPT4 P39504 bacterioph
 896 5 1.7 118 1 GHRL_FIG Q9gk5 sus scrofa
 897 5 1.7 118 1 NUT5_ARATH Q9xf5 arabidopsis
 898 5 1.7 119 1 C551_ROSDE P07625 roseobact
 899 5 1.7 119 1 E313_ADECU Q90094 canine aden
 900 5 1.7 119 1 HV3M_HUMAN P01774 homo sapien

ALIGNMENTS

RESULT 1
 M12A_HUMAN
 ID M12A_HUMAN STANDARD; PRT; 107 AA.
 AC P19575; Q9UPB8;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE Macrophage inflammatory protein-2-alpha precursor (MIP2-alpha) (CXCL2)
 DE (Growth regulated protein beta) (Gro-beta).
 GN CXCL2 OR GRO2 OR SCYB2 OR GROB OR MIP2A.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Histocytic lymphoma;
 RX MEDLINE=90354792; PubMed=2201751;
 RA Tekamp-Olsen P., Gallegos C., Bauer D., McClain J., Sherry B.,
 RA Fabre M., van Deventer S., Cerami A.;
 RT "Cloning and characterization of cDNAs for murine macrophage
 RT inflammatory protein 2 and its human homologues.";
 RL J. Exp. Med. 172:911-919(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90377259; PubMed=2078213;
 RA Iida N., Grotendorst G.R.;
 RT "Cloning and sequencing of a new gro transcript from activated human
 RT monocytes: expression in leukocytes and wound tissue.";
 RL Mol. Cell. Biol. 10:5596-5599(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91017578; PubMed=2217207;
 RA Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
 RA Smith T., Martin G., Ralph P., Sager R.;
 RT "Identification of three related human GRO genes encoding cytokine
 RT functions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Klausner R.D., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Stausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 35-107 FROM N.A.
 RA Jang J.S., Kim B.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP STRUCTURE BY NMR OF 39-107.
 RX MEDLINE=20069929; PubMed=10600366;
 RA Qian Y.O., Johanson K.O., McDewitt P.;
 RT "Nuclear magnetic resonance solution structure of truncated human
 RT GRObeta [5-73] and its structural comparison with CXCL chemokine
 RT family members GROalpha and IL-8.";
 RL J. Mol. Biol. 294:1065-1072(1999).
 CC -!- FUNCTION: Produced by activated monocytes and neutrophils and
 CC expressed at sites of inflammation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine CxCL2)
 CC family.
 CC -----
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 CC -----
 CC EMBL; X53799; CAA37808.1; -;
 DR EMBL; M36820; AAA63183.1; -;
 DR EMBL; M57731; AAA63182.1; -;
 DR EMBL; BC015753; AAH15753.1; -;
 DR EMBL; AF043340; AAC03540.1; -;
 DR PIR; JH0281; JH0281.
 DR PDB; 1QNK; 04-FEB-00.
 DR Genew; HGNC:4603; CXCL2.
 DR MIM; 139110; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008009; F:chemokine activity; TAS.
 DR GO; GO:0008935; P:chemotaxis; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR001811; Chemokine IL8.
 DR InterPro; IPR001089; CXCL2_cmkine_sm1.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCV; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
 FT 2-ALPHA.
 FT DISULFID 43 69
 FT DISULFID 45 85
 FT STRAND 49 49
 FT TURN 54 56
 FT STRAND 57 63
 FT STRAND 73 78
 FT TURN 79 80
 FT STRAND 83 86
 FT TURN 88 89
 FT TURN 93 95
 FT TURN 98 102
 SEQUENCE 107 AA; 11389 MW; 740F277E928571BA CRC64;

Query Match		2.8%; Score 8; DB 1; Length 107;	
Best Local Similarity		100.0%; Pred. No. 1.1;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	167 LLLVLAAS 174		
DB	22 LLLVLAAS 29		
RESULT 2			
ID	MI2B HUMAN	STANDARD;	PRT; 107 AA.
AC	P19876;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Macrophage inflammatory protein-2-beta precursor (MIP2-beta) (CXCL3)		
DE	(Growth regulated protein gamma) (GRO-gamma).		
GN	CXCL3 OR GRO3 OR SCYB3 OR GROG.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Histocytic lymphoma;		
RA	Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,		
RA	Fabre M., van Deventer S., Cerami A.;		
RT	"Cloning and characterization of cDNAs for murine macrophage		
RT	inflammatory protein 2 and its human homologues.";		
RL	J. Exp. Med. 172:911-919(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	MEDLINE=91017578; PubMed=2217207;		
RA	Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,		
RA	Smith T., Martin G., Ralph P., Sager R.;		
RT	"Identification of three related human GRO genes encoding cytokine		
RT	functions.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	MEDLINE=2238257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).		
CC	-!- FUNCTION: May play a role in inflammation and exert its effects on		
CC	endothelial cells in an autocrine fashion.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	-!- SIMILARITY: Belongs to the interleukin alpha (chemokine Cxcl)		
CC	family.		
CC	-----		
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or send an email to license@isb-sib.ch)			

CC	EMBL; X53800; CAA37809.1; -.		
DR	EMBL; M36821; AAG63184.1; -.		
DR	EMBL; BC016308; AAI16308.1; -.		
DR	PIR; JH0282; B38290.		
DR	HSSP; P19875; 1QNK.		
DR	Genew; HGNC:4604; CXCL3.		
DR	MIM; 139111; -.		
DR	GO; GO:0005615; C:extracellular space; TAS.		
DR	GO; GO:0008009; F:chemokine activity; TAS.		
DR	InterPro; IPR001811; Chemokine IL8.		
DR	InterPro; IPR001089; CXCL3_chmkine_sml.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.		
DR	Cytokine; Chemotaxis; Inflammatory response; Signal.		
KW	Signal		
FT	CHAIN 1 34		
FT	MACROPHAGE INFLAMMATORY PROTEIN-		
FT	2-BETA.		
FT	DISULFID 43 69		
FT	BY SIMILARITY.		
FT	DISULFID 45 85		
FT	BY SIMILARITY.		
FT	CONFLICT 27 28		
FT	AA -2 G (IN REP. 2).		
FT	SEQUENCE 107 AA; 11342 MW; 97A69946B7F1F070 CRC64;		
QY	Query Match	2.8%; Score 8; DB 1; Length 107;	
DB	Best Local Similarity	100.0%; Pred. No. 1.1;	
DB	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	167 LLLVLAAS 174		
DB	22 LLLVLAAS 29		
RESULT 3			
ID	SY04 MOUSE	STANDARD;	PRT; 92 AA.
AC	P14097;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory		
DE	protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).		
GN	CCL4 OR SCYA4 OR MIP1B.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	MEDLINE=89067830; PubMed=3058856;		
RA	Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,		
RA	Wolpe S.D., Masiarz F., Coit D., Cerami A.;		
RT	"Resolution of the two components of macrophage inflammatory protein		
RT	1, and cloning and characterization of one of those components,		
RT	macrophage inflammatory protein 1 beta.";		
RL	J. Exp. Med. 168:2251-2259(1988).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	MEDLINE=89093958; PubMed=2521353;		
RA	Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;		
RT	"A family of small inducible proteins secreted by leukocytes are		
RT	members of a new superfamily that includes leukocyte and fibroblast-		
RT	derived inflammatory agents, growth factors, and indicators of various		
RT	activation processes.";		
RL	J. Immunol. 142:679-687(1989).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DBA/2J; TISSUE=Liver;		

RA Dauberies P., Lepretre F., Bailloul B., Grove M., Pragnell I.,
 RA Plumb M.A.; Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=10.S/J, and SJL/J; TISSUE=Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
 RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis";
 RL J. Immunol. 163:2262-2266(1999).
 CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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 CC EMBL; M23503; AAA40148.1; -.
 DR EMBL; M35590; AAA39708.1; -.
 DR EMBL; X62502; CAA44364.1; -.
 DR EMBL; AF128218; AAF22559.1; -.
 DR EMBL; AF128219; AAF22560.1; -.
 DR PIR; C30552; C30552.
 DR HSP; P13236; IHUM.
 DR MGD; MGI:98261; Ccl4.
 DR InterPro; IPR000827; CC_chemokine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.
 FT DISULFID 34 58 BY SIMILARITY.
 FT DISULFID 35 74 BY SIMILARITY.
 SQ SEQUENCE 92 AA; 10168 MW; 8853FD58FDE61BAC CRC64;
 Query Match 2.4%; Score 7; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 LLLVAA 173
 Db 10 LLLVAA 16
 RESULT 4
 SY04 RAT
 ID SY04 RAT STANDARD; PRT; 92 AA.
 AC P50230;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 10-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
 DE protein 1-beta) (MIP-1-beta).
 GN CCL4 OR SCYA4 OR MIP1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Long Evans; TISSUE=Lung;
 RC

RA Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;
 RA Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=10.S/J, and SJL/J; TISSUE=Spleen;
 RX MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
 RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis";
 RL J. Immunol. 163:2262-2266(1999).
 CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
 CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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 CC EMBL; U06434; AAA36497.1; -.
 DR HSP; P13236; IHUM.
 DR InterPro; IPR000827; CC_chemokine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.
 FT DISULFID 34 58 BY SIMILARITY.
 FT DISULFID 35 74 BY SIMILARITY.
 SQ SEQUENCE 92 AA; 10234 MW; 60B451EBEBC7103D CRC64;
 Query Match 2.4%; Score 7; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 LLLVAA 173
 Db 10 LLLVAA 16
 RESULT 5
 GROG_BOVIN
 ID GROG_BOVIN STANDARD; PRT; 98 AA.
 AC C46675;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Growth regulated protein homolog gamma precursor (GRO-gamma).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99152612; PubMed=10028286;
 RA Modi W.S., Yoshimura T.;
 RT "Isolation of novel GRO genes and a phylogenetic analysis of the CXCR
 RT chemokine subfamily in mammals."
 RL Mol. Biol. Evol. 16:180-193(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CXCR)
 CC family.
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 CC EMBL; U95811; AAB93927.1; -.
 DR HSP; P19875; 1QNK.
 DR InterPro; IPR001811; Chemokine_IL8.

```
DR InterPro; IPR001089; CXc_chmkine_sm1.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR000437; SMALLCYTKCXC.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 98 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
FT SEQUENCE 98 AA; 10393 MW; 942CD6897C21EDE9 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 18 LLLLVAA 24

RESULT 6
GRO_SHEEP
ID GRO_SHEEP STANDARD; PRT; 103 AA.
AC O46578;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Growth regulated protein precursor (CXCL1).
DE Growth regulated protein precursor (CXCL1).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Medline=99152612; PubMed=10028286;
RA Modi W.S.; Yoshimura T.;
RT "Isolation of novel GRO genes and a phylogenetic analysis of the CXc
chemokine subfamily in mammals."
RL Mol. Biol. Evol. 16:180-193(1999).
CC -!- FUNCTION: Has chemotactic activity for neutrophils.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cx)
family.
CC
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CC
CC EMBL; U95814; AAB93930.1; -.
CC HSP; P19875; IONK.
CC InterPro; IPR001089; CXc_chmkine_sm1.
CC InterPro; IPR001089; CXc_chmkine_sm1.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR000437; SMALLCYTKCXC.
CC SMART; SM00199; SCV; 1.
CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 103 GROWTH REGULATED PROTEIN.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
FT SEQUENCE 103 AA; 10820 MW; C59857F346716695 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 18 LLLLVAA 24

RESULT 7
GRO2_RABIT
ID GRO2_RABIT STANDARD; PRT; 104 AA.
AC P47854;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Growth regulated protein homolog precursor (GRO homolog).
DE Growth regulated protein homolog precursor (GRO homolog).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz D.; Chaverri-Alamada L.; Berliner J.; Kirchgessner T.;
RA Quisomoro D.; Fang J.; Tekamp-Olson P.; Luis J.; Fogelman A.;
RA Territo M.;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: Plays a role in monocyte adhesion to the endothelium.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the Interleukin alpha (chemokine Cx)
family.
CC
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CC
CC EMBL; U12310; AAZ20487.1; -.
CC HSP; P19875; IONK.
CC InterPro; IPR001089; CXc_chmkine_sm1.
CC InterPro; IPR001089; CXc_chmkine_sm1.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR000437; SMALLCYTKCXC.
CC SMART; SM00199; SCV; 1.
CC PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 31 PROBABLE.
FT CHAIN 32 104 GROWTH REGULATED PROTEIN HOMOLOG.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
FT SEQUENCE 104 AA; 10900 MW; 10B9D07B65C77F67 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 19 LLLLVAA 25

RESULT 8
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 104 AA.
AC O46577;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Growth regulated protein homolog beta precursor (GRO-beta).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
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RX MEDLINE=95105175; PubMed=7806518;
RA Kim K.S., Clark-Iewis I., Sykes B.D.;
RT "Solution structure of GRO/melanoma growth stimulatory activity
RL determined by 1H NMR spectroscopy.";
CC J. Biol. Chem. 269:32909-32915(1994).
CC
CC -!- FUNCTION: Has chemotactic activity for neutrophils. May play a
CC role in inflammation and exerts its effects on endothelial cells
CC in an autocrine fashion.
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
CC -!- SIMILARITY: Belongs to the interleukin alpha (chemokine CXC)
CC family.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03561; AAA35933.1; -.
DR EMBL; X12510; CAA31027.1; -.
DR EMBL; X54489; CAA38361.1; -.
DR EMBL; BC011976; AAH11976.1; -.
DR PIR; S13669; A28414.
DR PDB; 1MSG; 30-SEP-94.
DR PDB; 1MSG; 31-MAR-95.
DR PDB; 1MSG; 31-MAR-95.
DR PDB; 1ROD; 10-JUN-96.
DR Gene; HGNC:4602; CXCL1.
DR MIM; 155730; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0008047; F:enzyme activator activity; TAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0007401; P:pan-neural process; TAS.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
DR SMART; SM0199; SCY; 1.
DR PROSITE; PS00471; SMALL CYTOKINES CXC; 1.
DR Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
KW SIGNAL
FT CHAIN 1 34 GROWTH REGULATED PROTEIN.
FT DISULFID 35 107
FT DISULFID 43 69
FT TURN 44 45
FT TURN 44 45
FT STRAND 49 49
FT TURN 54 56
FT STRAND 57 63
FT STRAND 73 78
FT STRAND 79 80
FT STRAND 83 86
FT TURN 88 89
FT HELIX 91 103
FT TURN 104 104
SQ SEQUENCE 107 AA; 11301 MW; 17048A6B4D765CA2 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 22 LLLLVAA 28

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RESULT 10
YB76 AQUAE STANDARD; PRT; 111 AA.
ID YB76 AQUAE STANDARD; PRT; 111 AA.
AC O67237;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1176.
GN AQ_1176.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -----
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CC -----
DR EMBL; AE000727; AAC07206.1; -.
DR PIR; B70401; B70401.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 111 AA; 12958 MW; C38490CB2FF25B19 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 DOVEVEY 236
DB 38 DOVEVEY 44

RESULT 11
LY96 CRIGR STANDARD; PRT; 160 AA.
ID LY96 CRIGR STANDARD; PRT; 160 AA.
AC P58755;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphocyte antigen 96 precursor (MD-2 protein).
GN LY96 OR MD2.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT TYR-95.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=21329173; PubMed=11435474;
RA Schramm A.B., Lien E., Henneke P., Chow J.C., Yoshimura A., Heine H.,
RA Latz E., Monks B.G., Schwartz D.A., Miyake K., Golenbock D.T.;
RT "Molecular genetic analysis of an endotoxin nonresponder mutant cell
RT line. A point mutation in a conserved region of MD-2 abolishes
RT endotoxin-induced signaling.";
RL J. Exp. Med. 194:79-88(2001).
CC -!- FUNCTION: Cooperates with TLR4 in the innate immune response to
CC bacterial lipopolysaccharide (LPS), and with TLR2 in the response

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to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS (BY similarity).

-!- SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least Cbl4, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (BY similarity).

-!- SUBCELLULAR LOCATION: Extracellular.

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EMBL; AF325501; AKS7984.1; -
 InterPro; IPR003172; E1_DerP2_DerF2.
 InterPro; IPR007110; IG-Like.
 Pfam; PF02221; E1_DerP2_DerF2; 1.
 SMART; SM00737; ML; 1.
 Immune response; Inflammatory response; Signal; Glycoprotein;
 Polymorphism.

FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 160 LYMPHOCYTE ANTIGEN 96.
 FT DISULFID 95 105 BY SIMILARITY.
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 95 95 C -> Y (IN ENDOTOXIN NONRESPONDER).
 FT SEQUENCE 160 AA; 18357 MW; 0E533B1AA5B46DD6 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 160;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 LPLIFT 164
 DB 10 LPLIFT 16

RESULT 12
 YW87_PSEAE
 ID_YW87_PSEAE STANDARD; PRT; 171 AA.
 AC Q9HV6,
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical ANK-repeat protein PA3287.
 GN PA3287.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.H., Huhnagel W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goulet S.N., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RI Nature 406:959-964(2000).
 CC -!- SIMILARITY: Contains 3 ANK repeats.

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EMBL; AEO04751; AAG06675.1; -
 PIR; H83233; H83233.
 InterPro; IPR002110; ANK.
 Pfam; PF00023; ank; 4.
 SMART; SM00248; ANK; 3.
 PROSITE; PSS0088; ANK_REPEAT; 3.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 KW Hypothetical protein; Repeat; ANK repeat; Complete proteome.
 FT REPEAT 48 77
 FT REPEAT 81 110 ANK 2.
 FT REPEAT 114 143 ANK 3.
 FT SEQUENCE 171 AA; 18194 MW; 16C0C8A47120E03C CRC64;

Query Match 2.4%; Score 7; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 VAASLLA 177
 DB 130 VAASLLA 136

RESULT 13
 FARP_CAEEL
 ID_FARP_CAEEL STANDARD; PRT; 175 AA.
 AC P41855;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE FMRamide-like neuropeptides precursor.
 GN FLP-1 OR F23B2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC STRAIN=Bristol N2;
 RX MEDLINE=92300457; PubMed=1607945;
 RA Rosoff M.L., Bueglin T.R., Li C.;
 RT "Alternatively spliced transcripts of the flp-1 gene encode distinct
 RT FMRamide-like peptides in Caenorhabditis elegans.";
 RL J. Neurosci. 12:2356-2361(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA McMurray A.A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=93248060; PubMed=8483810;
 RA Rosoff M.L., Doble K.E., Price D.A., Li C.;
 RT "The flp-1 propeptide is processed into multiple, highly similar
 RT FMRamide-like peptides in Caenorhabditis elegans.";
 RL Peptides 14:331-338(1993).
 CC -!- FUNCTION: May function as a hormone.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P41855-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P41855-2; Sequence=VSP_001563;
 CC Note=Expressed at about a twofold higher level than isoform
 CC Long;
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)

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CC family.
CC -----
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CC -----
CC EMBL; S38096; AAC223368.1; --
CC EMBL; U00670; AAC46464.1; --
CC EMBL; Z82266; CAB05179.1; --
CC PIR; B44827; B44827.
CC PIR; T21297; T21297.
CC WormPep; F23B2.5; CB09585.
CC InterPro; IPR002544; 8.
CC Pfam; PF01581; FARP; 8.
CC Neuropeptide; Amidation; Repeat; Signal; Alternative splicing.
CC SIGNAL 1 21
CC PROPEP 22 67
CC PEPTIDE 71 76 PNFVRY-AMIDE.
CC PROPEP 79 86
CC PEPTIDE 89 98 AGSDPNFLRF-AMIDE.
CC PEPTIDE 101 108 SGNFLRF-AMIDE.
CC PEPTIDE 111 120 ASGDPNFLRF-AMIDE.
CC PEPTIDE 123 130 SDPNFLRF-AMIDE (PF1).
CC PEPTIDE 133 142 AAADPNFLRF-AMIDE.
CC PROPEP 146 154 SADPNFLRF-AMIDE (PF2).
CC PEPTIDE 157 165
CC PEPTIDE 168 173 PNFNRF-AMIDE.
CC MOD RES 76 76 AMIDATION (G-77 PROVIDE AMIDE GROUP).
CC MOD RES 98 98 AMIDATION (G-99 PROVIDE AMIDE GROUP).
CC MOD RES 108 108 AMIDATION (G-109 PROVIDE AMIDE GROUP).
CC MOD RES 120 120 AMIDATION (G-121 PROVIDE AMIDE GROUP).
CC MOD RES 130 130 AMIDATION (G-131 PROVIDE AMIDE GROUP).
CC MOD RES 142 142 AMIDATION (G-143 PROVIDE AMIDE GROUP).
CC MOD RES 154 154 AMIDATION (G-155 PROVIDE AMIDE GROUP).
CC MOD RES 173 173 AMIDATION (G-174 PROVIDE AMIDE GROUP).
CC VARSPPLIC 81 Missing (in isoform Short).
CC FT FTId=VSP 001563.
CC SEQUENCE 175 AA; 19705 MW; 9588DF266B59E7F CRC64;

Query Match 2.4%; Score 7; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLLVAA 173
DB 9 LLLLVAA 15
|||||

RESULT 14
RRF_NEIMA
ID_RRF_NEIMA STANDARD; PRT; 185 AA.
AC Q9UR52;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome recycling factor (Ribosome releasing factor) (RRF).
GN RRF OR NMA0080 OR NMB0187.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

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RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL meningitidis Z2491."
RN Nature 404:502-506(2000).
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittiore K., Clark E.B.,
RA Cotton M.D., Utterback T.R., Knouri H., Qin H., Vamathevan J.,
RA Gill J., Scariato V., Masignani V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RL MC58."
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Responsible for the release of ribosomes from messenger
CC RNA at the termination of protein biosynthesis. May increase the
CC efficiency of translation by recycling ribosomes from one round of
CC translation to another (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the RRF family.
CC -----
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CC -----
CC EMBL; AL162752; CAB83396.1; --
CC EMBL; AR002375; AAF40644.1; --
CC PIR; D81229; D81229.
CC HSSP; Q9X1B9; 1DD5.
CC TIGR; NMB0187; --
CC HAMAP; MF_00040; --
CC InterPro; IPR002661; RRF.
CC Pfam; PF01765; RRF; 1.
CC ProDom; PD004103; RRF; 1.
CC TIGRFAMs; TIGR00496; frr; 1.
CC Protein biosynthesis; Complete proteome.
KW SEQUENCE 185 AA; 20731 MW; 668D1C347B846603 CRC64;

Query Match 2.4%; Score 7; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 DOVEVEY 236
DB 38 DOVEVEY 44
|||||

RESULT 15
HA19_MOUSE
ID_HA19_MOUSE STANDARD; PRT; 200 AA.
AC P14431;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE H-2 class I histocompatibility antigen, Q9 alpha chain precursor
DE (Fragment).
GN H2-Q9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10;
RX MEDLINE=86135949; PubMed=3004940;
RA Devlin J.J., Weiss E.H., Paulson M., Flavell R.A.;
RT "Duplicated gene pairs and alleles of class I genes in the Qa2 region
of the murine major histocompatibility complex: a comparison.";
RL EMBO J. 4:3203-3207(1985).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC -----
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CC -----
CC EMBL: X03443; CAA27172.1; ALT_INIT.
DR HSP; P16391; 1ED3.
DR MGD; MG1:95938; H2-Q9.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASS1.
DR ProDom; PD000050; MHC_I; 1.
DR PROSITE; PS00290; IG_MHC; PARTIAL.
KW MHC I; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 >200
FT -----
FT H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT Q9 ALPHA CHAIN.
FT DOMAIN 22 111
FT DOMAIN 112 >200
FT DISULFID 122 185
FT CARBOHYD 107 107
FT NON_TER 200 200
FT SEQUENCE 200 AA; 23025 MW; 4C2B7E2D059EA82E CRC64;
QY 167 LLLLVAA 173
DB 6 LLLLVAA 12
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Query Match 2.4%; Score 7; DB 1; Length 200;
Best Local Similarity 100.0%; Pred.No.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: September 16, 2004, 12:52:35
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2004, 12:48:26 / Search time 116 Seconds
(without alignments)
788.796 Million cell updates/sec

Title: US-09-997-131-65

Perfect score: 290

Sequence: 1 MPLLTYLLFWLSGYSIAT.....SXLPGRGPETPEYSTISRP 290

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTRMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	57.2	290	4	Q726A6
2	149	51.4	244	4	Q8NAP5
3	137	47.2	290	4	Q8TD01
4	134	46.2	194	4	Q8N6D0
5	120	41.4	293	4	Q72715
6	71	24.5	165	4	Q72714
7	10	3.4	201	4	Q8IX40
8	10	3.4	238	4	Q8N6D1
9	9	3.1	472	16	Q7WEK0
10	9	3.1	472	16	Q7W381
11	9	3.1	545	10	Q8S1L2
12	9	3.1	1102	16	Q88CW3
13	9	3.1	3956	2	Q7WTF2
14	8	2.8	149	13	O57313
15	8	2.8	186	4	Q3UMT0
16	8	2.8	221	11	Q8BRU3

221	11	Q8VCH2	Q8vch2 mus musculu
264	16	Q88NT2	Q88nt2 pseudomonas
283	11	Q8K4V9	Q8k4v9 mus musculu
298	4	Q9HD97	Q9hd97 homo sapien
299	4	Q9UGN4	Q9ugn4 homo sapien
299	4	Q9UBK4	Q9ubk4 homo sapien
301	4	Q9S100	Q9s100 homo sapien
374	10	Q8SBD0	Q8sbd0 oryza sativ
395	16	Q89ZL3	Q89zl3 bacteroides
475	16	Q8YM67	Q8ym67 anabaena sp
484	16	Q9KYG5	Q9kyg5 streptomyce
600	17	Q980K5	Q980k5 sulfobolus
674	10	Q94E29	Q94e29 oryza sativ
695	5	Q86LL4	Q86ll4 giardia lam
708	5	P91954	P91954 lucilia cup
813	16	Q8XZJ7	Q8xzz7 raietonia s
24	7	Q861J2	Q861j2 rattus norv
36	16	Q8F1V7	Q8f1v7 leptospira
64	16	Q89DM0	Q89dm0 bradyrhizob
76	10	Q84PU7	Q84pu7 oryza sativ
80	2	Q9RHX1	Q9rthx1 corynebacte
91	16	Q825L2	Q825l2 streptomyce
99	17	Q97Z64	Q97z64 sulfobolus
109	11	Q60639	Q60639 mus musculu
109	11	Q62653	Q62653 rattus norv
120	16	Q91YW2	Q91yw2 neisseria m
120	16	Q9A4P5	Q9a4p5 caulobacter
125	2	O53123	O53123 mycobacteri
142	5	Q81122	Q81122 caenorhabdi
145	8	Q94QD8	Q94qd8 crotalus tr
145	16	Q9KQ01	Q9kq01 vibrio chol
151	10	Q9FFX3	Q9ffy3 arabidopsis
158	16	Q7VX71	Q7vx71 bordetella
162	16	Q7WLI4	Q7wli4 bordetella
162	16	Q7W837	Q7w837 bordetella
164	5	Q23805	Q23805 caenorhabdi
164	10	Q8LI24	Q8li24 oryza sativ
166	2	Q7XD76	Q7xd76 bacillus th
167	2	Q7X0E5	Q7x0e5 staphylococ
167	2	Q7X0E4	Q7x0e4 staphylococ
167	10	Q8LDL5	Q8ldl5 arabidopsis
167	10	Q9SAC5	Q9sac5 arabidopsis
172	15	Q86689	Q86689 feline immu
172	15	Q9PKX9	Q9pkx9 feline immu
174	5	Q23806	Q23806 caenorhabdi
184	7	Q9CZ20	Q9cz20 mus musculu
187	17	Q9YER3	Q9yer3 aeropyrum p
190	2	Q93D74	Q93d74 bacillus th
190	5	Q9GYC2	Q9gyc2 leishmania
192	16	Q8ZNI5	Q8zni5 salmonella
194	16	Q9A9U0	Q9a9u0 caulobacter
198	10	Q9ARPI	Q9arp1 oryza sativ
198	10	Q7XXK6	Q7xxk6 oryza sativ
202	10	Q8GW95	Q8gw95 arabidopsis
208	5	Q8SV33	Q8sv33 encephalito
210	2	Q938B2	Q938b2 anaplaema c
210	16	Q55649	Q55649 synechocyst
215	16	Q98H67	Q98h67 rhizobium l
218	5	Q9TZF3	Q9tzf3 caenorhabdi
222	10	Q8L472	Q8l472 oryza sativ
230	2	Q8XK71	Q8xk71 aeromonas h
233	2	Q8RR77	Q8rr77 staphylococ
233	16	Q83CV2	Q83cv2 coxiella bu
244	16	Q88YAS	Q88yas lactobacill
244	16	Q84RWO	Q84rwo oryza sativ
253	10	Q8EHF5	Q8ehf5 shewanella
253	16	Q89C05	Q89cg5 bradyrhizob
256	16	Q9UCG4	Q9ucz4 pyrococcus
257	17	Q9ZNM3	Q9znm3 staphylococ
258	2	Q9ZNF2	Q9znf2 staphylococ
260	5	Q8T0Z3	Q8t0z3 triatoma in
265	16	Q98DT6	Q98dt6 rhizobium l
270	11	Q8R159	Q8r159 mus musculu

90	7	2.4	273	2	O68480	O68480 achromobact	163	7	2.4	452	11	Q8BN13	Q8bn13 mus musculus
91	7	2.4	283	16	O8F57	O8f5w7 leptospira	164	7	2.4	462	16	Q88AT3	Q88at3 pseudomonas
92	7	2.4	283	16	O8E89	O8e8k9 shewanella	165	7	2.4	464	16	Q8E8T1	Q8e8t1 shewanella
93	7	2.4	284	16	O8RV15	O8rv15 delnoccocus	166	7	2.4	465	10	Q8LJ43	Q8lj43 oryza sativ
94	7	2.4	284	16	O8YCN9	O8ycn9 brucella me	167	7	2.4	468	16	Q8WH5	Q8wh5 bordetella
95	7	2.4	287	16	O8K877	O8k877 bacillus ha	168	7	2.4	468	16	Q8VHS9	Q8vhs9 bordetella
96	7	2.4	289	3	Q01090	Q01090 kluyveromye	169	7	2.4	476	4	Q8Y224	Q8y224 homo sapien
97	7	2.4	290	16	O8AL80	O8al80 brucella su	170	7	2.4	477	4	Q8YH17	Q8yh17 homo sapien
98	7	2.4	292	16	O8Y176	O8y1t6 ralstonia s	171	7	2.4	478	16	Q8LRW3	Q8lrw3 bacillus an
99	7	2.4	293	16	O8O896	O8o8s6 salcomella	172	7	2.4	480	10	Q8S2L2	Q8s2l2 oryza sativ
100	7	2.4	295	13	Q8J132	Q8j132 encornynchu	173	7	2.4	500	16	Q8KD12	Q8kd12 chlorobium
101	7	2.4	299	16	Q8I092	Q8i092 pseudomonas	174	7	2.4	508	12	Q8S579	Q8s579 bovine herp
102	7	2.4	301	16	O82NH5	O82nh5 streptomyce	175	7	2.4	508	12	Q8S821	Q8s821 bovine herp
103	7	2.4	304	4	Q8NEP4	Q8nep4 homo sapien	176	7	2.4	519	16	Q82708	Q82708 heliamydia p
104	7	2.4	308	16	O89F70	O89fj0 bradyrhizob	177	7	2.4	520	10	O65815	O65815 helianthus
105	7	2.4	309	16	O89V74	O89v74 staphylococ	178	7	2.4	521	6	O46651	O46651 cryctolagus
106	7	2.4	311	17	Q8Y8U7	Q8y8u7 aeropyrum p	179	7	2.4	521	6	O46634	O46634 canis famil
107	7	2.4	312	2	Q8VQ59	Q8vq59 staphylococ	180	7	2.4	522	16	Q8G2H8	Q8g2h8 brucella su
108	7	2.4	312	16	O8ERN3	O8ern3 bradyrhizob	181	7	2.4	524	10	Q8GTK2	Q8gtk2 oryza sativ
109	7	2.4	314	11	Q7TSN3	Q7tsn3 mus musculus	182	7	2.4	533	16	Q8YFE2	Q8yfe2 brucella me
110	7	2.4	318	11	O8CFN3	O8cfn3 mus musculus	183	7	2.4	533	17	Q8V0J2	Q8v0j2 pyrococcus
111	7	2.4	318	11	Q7TNS6	O7tns6 mus musculus	184	7	2.4	537	2	Q8EZ98	Q8ez98 zymomonas m
112	7	2.4	319	16	O8CFI8	O8cfi8 lactococcus	185	7	2.4	538	16	Q8KRN1	Q8krn1 vibrio chol
113	7	2.4	320	16	O82L57	O82lb7 streptomyce	186	7	2.4	539	5	Q8T4G6	Q8t4g6 drosophila
114	7	2.4	324	2	Q8KIK7	Q8kik7 rhizobium e	187	7	2.4	539	10	Q8LN93	Q8ln93 arabidopsis
115	7	2.4	326	7	P79567	P79567 mus musculus	188	7	2.4	539	16	Q8RD59	Q8rd59 streptomyce
116	7	2.4	326	7	P79568	P79568 mus musculus	189	7	2.4	539	16	Q87P06	Q87p06 vibrio para
117	7	2.4	327	17	Q9V2H9	Q9v2h9 pyrococcus	190	7	2.4	543	2	Q8L868	Q8l868 desulfovibr
118	7	2.4	328	7	Q31199	Q31199 mus musculus	191	7	2.4	543	16	Q8P8R5	Q8p8r5 xanthomonas
119	7	2.4	329	12	O8JP87	O8jp87 corriparta	192	7	2.4	547	5	Q9VD53	Q9vd53 drosophila
120	7	2.4	331	2	O87492	O87492 staphylococ	193	7	2.4	549	10	Q8LN87	Q8ln87 arabidopsis
121	7	2.4	331	16	Q99XA0	Q99xa0 staphylococ	194	7	2.4	550	4	Q8N4X7	Q8n4x7 homo sapien
122	7	2.4	331	16	O8ERC2	O8erc2 thermoanaer	195	7	2.4	554	15	Q8SD93	Q8sd93 pseudomonas
123	7	2.4	331	16	O8NYG8	O8nyg8 staphylococ	196	7	2.4	557	9	Q8IH53	Q8ih53 drosophila
124	7	2.4	331	16	O8NR33	O8nr33 corynebacte	197	7	2.4	558	5	Q8T0S1	Q8t0s1 xenopus lae
125	7	2.4	336	2	Q7X222	Q7x222 uncultured	198	7	2.4	560	13	Q7T0S1	Q7t0s1 xenopus lae
126	7	2.4	338	16	O8R908	O8r908 rhizobium m	199	7	2.4	561	11	Q8BPC8	Q8bpc8 mus musculus
127	7	2.4	341	13	Q90WF6	Q90wf6 gallus gall	200	7	2.4	561	16	Q82BG1	Q82bg1 streptomyce
128	7	2.4	341	13	Q90644	Q90644 gallus gall	201	7	2.4	562	3	Q8VVB9	Q8vvb9 pichia cife
129	7	2.4	345	2	Q8L2N0	Q8l2n0 bacillus th	202	7	2.4	563	11	Q8BI72	Q8bi72 mus musculus
130	7	2.4	349	5	Q95Y11	Q95y11 caenorhabdi	203	7	2.4	570	4	Q8N821	Q8n821 homo sapien
131	7	2.4	357	16	O7TY47	O7ty47 mycobacteri	204	7	2.4	572	10	Q8VYV8	Q8vyv8 arabidopsis
132	7	2.4	358	17	O970G1	O970g1 sulfobobus	205	7	2.4	579	4	Q8TBM5	Q8tbm5 homo sapien
133	7	2.4	363	11	O8BI61	O8bi61 mus musculus	206	7	2.4	580	4	Q9NXV6	Q9nxv6 homo sapien
134	7	2.4	363	17	Q97BE1	Q97be1 thermoplasm	207	7	2.4	588	16	Q8PMA4	Q8pma4 xanthomonas
135	7	2.4	366	10	Q93Y71	Q93y71 oryza sativ	208	7	2.4	592	16	Q83A98	Q83a98 coxiella bu
136	7	2.4	372	2	Q86182	Q86182 streptomyce	209	7	2.4	593	4	Q7Z3F9	Q7z3f9 homo sapien
137	7	2.4	373	7	Q861Q1	Q861q1 rattus norv	210	7	2.4	595	12	Q83896	Q83896 ovine adeno
138	7	2.4	378	16	O8DJ31	O8djl1 synecococc	211	7	2.4	596	17	Q8TRM8	Q8trm8 methanosarc
139	7	2.4	380	16	O8ZHI7	O8zhl7 versinia pe	212	7	2.4	598	3	Q871F6	Q871f6 neurospora
140	7	2.4	387	3	Q86ZX7	Q86zx7 conidiobolu	213	7	2.4	598	16	Q8PHX4	Q8phx4 xanthomonas
141	7	2.4	391	17	Q97983	Q97983 thermoplasm	214	7	2.4	598	17	Q29907	Q29907 archaetoglob
142	7	2.4	394	16	O7V1F4	O7v1f4 prochloroco	215	7	2.4	599	16	Q8KAF2	Q8kaf2 bacillus ha
143	7	2.4	400	5	Q9BJM2	Q9bjm2 litomosoid	216	7	2.4	600	16	Q8F6M0	Q8f6m0 xanthomonas
144	7	2.4	401	5	Q968A6	Q968a6 plasmodium	217	7	2.4	600	16	Q89Q33	Q89q33 bradyrhizob
145	7	2.4	407	16	O8XU94	O8xu94 ralstonia s	218	7	2.4	617	11	O54766	O54766 rattus norv
146	7	2.4	410	16	Q9RJ38	Q9rj38 streptomyce	219	7	2.4	627	16	Q7UQW4	Q7uqw4 rhodopirell
147	7	2.4	412	2	Q7WV93	Q7wv93 alcaligenes	220	7	2.4	631	4	Q8NVH0	Q8nyh0 homo sapien
148	7	2.4	414	16	Q8XU02	Q8xu02 ralstonia s	221	7	2.4	634	4	Q8TAE4	Q8tae4 homo sapien
149	7	2.4	415	10	Q9AS33	Q9as33 oryza sativ	222	7	2.4	634	11	Q8BTU3	Q8btu3 mus musculus
150	7	2.4	416	16	O67172	O67172 aquifex aeo	223	7	2.4	635	4	Q869Y5	Q869y5 homo sapien
151	7	2.4	417	16	O7TYQ0	O7tyq0 mycobacteri	224	7	2.4	642	16	O25396	O25396 helicobacte
152	7	2.4	419	16	O986W4	O986w4 rhizobium l	225	7	2.4	642	16	Q9ZLF3	Q9zlf3 helicobacte
153	7	2.4	421	16	O98L27	O98l27 rhizobium l	226	7	2.4	652	5	Q9W0G4	Q9w0g4 drosophila
154	7	2.4	422	2	Q8F826	Q8f826 micromonosp	227	7	2.4	652	2	Q93D79	Q93d79 bacillus th
155	7	2.4	422	16	Q8K7F0	Q8k7f0 bacillus ha	228	7	2.4	658	16	Q8P3D2	Q8p3d2 xanthomonas
156	7	2.4	430	16	P71757	P71757 mycobacteri	229	7	2.4	661	5	Q9M185	Q9m185 drosophila
157	7	2.4	441	4	Q86UN2	Q86un2 homo sapien	230	7	2.4	662	5	Q84R58	Q84r58 drosophila
158	7	2.4	444	10	O8H3C8	O8h3c8 oryza sativ	231	7	2.4	665	2	Q845T2	Q845t2 vibrio vuln
159	7	2.4	445	5	Q9W478	Q9w478 drosophila	232	7	2.4	665	16	Q8D5B0	Q8d5b0 vibrio vuln
160	7	2.4	449	2	Q93EJ5	Q93ej5 bacillus li	233	7	2.4	675	8	Q9TAJ6	Q9taj6 caferteria r
161	7	2.4	452	11	Q9DD22	Q9dd22 mus musculus	234	7	2.4	687	5	Q8SKR7	Q8skr7 drosophila
162	7	2.4	452	11	Q99LJ1	Q99lj1 mus musculus	235	7	2.4	687	10	Q948Y7	Q948y7 volvox cart

236	7	2.4	694	11	Q8CFT6	Q8cft6 mus musculus	309	7	2.4	4283	11	Q9ERV0	Q9erv0 rattus norv
237	7	2.4	697	5	Q8IH79	Q8ih79 drosophila	310	7	2.4	4368	5	Q61851	Q61851 caenorhabdi
238	7	2.4	704	5	Q95XQ7	Q95xq7 caenorhabdi	311	7	2.4	4717	3	Q94248	Q94248 schizosacch
239	7	2.4	707	11	Q8QW65	Q8Qw65 mus musculus	312	6	2.1	10	12	Q39958	Q39958 hepatitis g
240	7	2.4	722	16	Q8DHZ8	Q8dhz8 synechococc	313	6	2.1	23	9	Q8W5S4	Q8w5s4 bacterioph
241	7	2.4	724	16	Q87BR9	Q87br9 xylella fas	314	6	2.1	27	2	Q44952	Q44952 borrelia bu
242	7	2.4	751	12	Q93294	Q93294 equine herp	315	6	2.1	28	8	Q9G6G3	Q9g6g3 tympanocryp
243	7	2.4	756	16	Q8CVDU1	Q8cvm1 pasteurella	316	6	2.1	29	2	Q9R4D5	Q9r4d5 eubacterium
244	7	2.4	763	16	Q8EAB7	Q8eab7 shewanella	317	6	2.1	30	16	Q8EAT6	Q8eat6 shewanella
245	7	2.4	766	4	Q8NB10	Q8nb10 homo sapien	318	6	2.1	32	12	Q9FWS8	Q9fws8 sindbis vir
246	7	2.4	789	10	Q9FWJ2	Q9fmj2 arabidopsis	319	6	2.1	33	10	Q94IS3	Q94is3 pinus radia
247	7	2.4	788	16	Q827F5	Q827f5 streptomyce	320	6	2.1	34	2	Q8R529	Q8r529 escherichia
248	7	2.4	789	2	Q45793	Q45793 bacillus th	321	6	2.1	36	8	Q85FL2	Q85fl2 adiantum ca
249	7	2.4	789	2	Q59270	Q59270 bacillus th	322	6	2.1	39	2	Q9RIJ8	Q9rij8 streptococc
250	7	2.4	789	2	Q45792	Q45792 bacillus th	323	6	2.1	40	10	Q94IS0	Q94is0 pinus radia
251	7	2.4	789	2	Q8RS25	Q8rs25 bacillus th	324	6	2.1	50	10	Q41532	Q41532 triticum ae
252	7	2.4	789	2	Q938Z1	Q938z1 bacillus th	325	6	2.1	50	12	Q8Z053	Q8z053 hepatitis g
253	7	2.4	797	4	Q96B75	Q96b75 homo sapien	326	6	2.1	50	12	Q8Z046	Q8z046 hepatitis g
254	7	2.4	801	16	Q8CPU8	Q8cpu8 staphylococ	327	6	2.1	51	15	Q9QGE7	Q9qge7 human immun
255	7	2.4	802	5	Q95QC4	Q95qc4 caenorhabdi	328	6	2.1	52	4	Q8NHT5	Q8nht5 homo sapien
256	7	2.4	812	4	Q8NOM6	Q8nom6 homo sapien	329	6	2.1	53	16	Q8ZRC7	Q8zrc7 salmonella
257	7	2.4	824	10	Q8LV73	Q8lv73 arabidopsis	330	6	2.1	55	16	Q87FG1	Q87fg1 vibrio para
258	7	2.4	837	5	Q8T2A5	Q8t2a5 dictyosteli	331	6	2.1	58	9	Q03908	Q03908 bacterioph
259	7	2.4	849	10	Q7XSS2	Q7xss2 oryza sativ	332	6	2.1	59	5	Q61591	Q61591 osteretgia
260	7	2.4	878	16	Q99ZP1	Q99zf1 streptococc	333	6	2.1	59	10	Q9SBC7	Q9sbc7 leavenworth
261	7	2.4	878	16	Q8P0U3	Q8p0u3 streptococc	334	6	2.1	59	10	Q81686	Q81686 leavenworth
262	7	2.4	878	16	Q8K7B4	Q8k7b4 streptococc	335	6	2.1	59	10	Q81681	Q81681 leavenworth
263	7	2.4	890	4	Q8N277	Q8n277 homo sapien	336	6	2.1	59	10	Q82815	Q82815 leavenworth
264	7	2.4	900	16	Q92Z67	Q92z67 rhizobium m	337	6	2.1	59	10	Q81678	Q81678 leavenworth
265	7	2.4	909	4	Q8N3F3	Q8nf3 homo sapien	338	6	2.1	59	10	Q81683	Q81683 leavenworth
266	7	2.4	925	2	Q9F4U0	Q9f4j0 porphyronon	339	6	2.1	59	10	Q81684	Q81684 leavenworth
267	7	2.4	929	4	Q8N973	Q8n973 homo sapien	340	6	2.1	59	10	Q81687	Q81687 leavenworth
268	7	2.4	969	4	Q86V43	Q86v43 homo sapien	341	6	2.1	59	10	Q81682	Q81682 leavenworth
269	7	2.4	985	2	Q9ZNI6	Q9zni6 pseudomonas	342	6	2.1	59	10	Q81685	Q81685 leavenworth
270	7	2.4	988	10	Q9FWV2	Q9fwv2 oryza sativ	343	6	2.1	59	10	Q85773	Q85773 catharanthu
271	7	2.4	988	10	Q7XD45	Q7xd45 oryza sativ	344	6	2.1	61	10	Q9C5B7	Q9c5b7 arabidopsis
272	7	2.4	1009	16	Q8U8W1	Q8u8w1 agrobacteri	345	6	2.1	62	4	Q8WX05	Q8wx05 homo sapien
273	7	2.4	1010	16	Q9X8M9	Q9x8m9 streptomyce	346	6	2.1	62	5	Q7YVA8	Q7yva8 trypanosoma
274	7	2.4	1013	4	Q9NT81	Q9nt81 homo sapien	347	6	2.1	62	16	Q98NP7	Q98np7 rhizobium l
275	7	2.4	1015	4	Q8N3X1	Q8n3x1 homo sapien	348	6	2.1	64	9	Q9XJS2	Q9xjs2 bacterioph
276	7	2.4	1023	5	Q9XYD4	Q9xyd4 dictyosteli	349	6	2.1	65	2	Q9FCZ0	Q9fcz0 erwinia ste
277	7	2.4	1050	4	Q9Y2L7	Q9y2l7 homo sapien	350	6	2.1	65	2	Q85378	Q85378 lactococcus
278	7	2.4	1058	11	Q9QY84	Q9qys4 mus musculus	351	6	2.1	65	16	Q8YGM2	Q8ygm2 brucella me
279	7	2.4	1058	11	Q9QZK2	Q9qz2 mus musculus	352	6	2.1	65	16	Q8GL93	Q8gl93 brucella su
280	7	2.4	1058	11	Q8CDH7	Q8cdh7 mus musculus	353	6	2.1	66	11	Q9QWE3	Q9qwe3 mus sp. alp
281	7	2.4	1060	5	Q86AN6	Q86an6 dictyosteli	354	6	2.1	66	17	Q9YCD4	Q9ycd4 aeropyrum p
282	7	2.4	1063	5	Q9U699	Q9u699 drosophila	355	6	2.1	68	5	Q8VNR7	Q8vmr7 caenorhabdi
283	7	2.4	1063	5	Q9TVM2	Q9tvm2 drosophila	356	6	2.1	68	16	Q8AAD1	Q8aad1 bacteroides
284	7	2.4	1067	16	Q8RZQ3	Q8rzq3 deingococcus	357	6	2.1	70	5	Q9BPA9	Q9bpa9 conus texti
285	7	2.4	1089	16	Q9HTT4	Q9htt4 pseudomonas	358	6	2.1	71	5	Q9BPA7	Q9bpa7 conus penna
286	7	2.4	1103	5	Q97721	Q97721 plasmodium	359	6	2.1	72	5	Q9BPA1	Q9bpa1 conus texti
287	7	2.4	1151	5	Q96993	Q96993 heterodera	360	6	2.1	72	10	Q8S9N3	Q8s9n3 oryza sativ
288	7	2.4	1184	16	Q05435	Q05435 mycobacteri	361	6	2.1	73	2	Q9X5W9	Q9x5w9 pantoea cit
289	7	2.4	1184	16	Q7TVD1	Q7tvd1 mycobacteri	362	6	2.1	73	5	Q9BPA4	Q9bpa4 conus texti
290	7	2.4	1185	11	Q8CHA4	Q8cha4 mus musculus	363	6	2.1	73	5	Q9BPA2	Q9bpa2 conus texti
291	7	2.4	1208	5	Q815T3	Q815t3 plasmodium	364	6	2.1	73	5	Q9BPA5	Q9bpa5 conus texti
292	7	2.4	1228	5	Q97724	Q97724 plasmodium	365	6	2.1	73	16	Q8Y1A1	Q8y1a1 ralstonia s
293	7	2.4	1242	3	Q60103	Q60103 schizosacch	366	6	2.1	74	5	Q9BPD0	Q9bpd0 conus ventr
294	7	2.4	1264	5	Q9U445	Q9u445 plasmodium	367	6	2.1	74	5	Q9BPC9	Q9bpc9 conus ventr
295	7	2.4	1332	16	Q8PFO6	Q8pfq6 xanthomonas	368	6	2.1	75	5	Q9BPC9	Q9bpc9 conus tessu
296	7	2.4	1399	5	Q7YVJ2	Q7yvjl2 trypanosoma	369	6	2.1	76	2	Q93A63	Q93a63 gamma-prote
297	7	2.4	1430	13	Q7Z288	Q7z288 brachydanio	370	6	2.1	76	2	Q9BPA8	Q9bpa8 conus texti
298	7	2.4	1498	5	Q7YZS4	Q7yzs4 physarum po	371	6	2.1	76	5	Q9BPC6	Q9bpc6 conus ventr
299	7	2.4	1540	10	Q9SGX4	Q9sgx4 arabidopsis	372	6	2.1	76	5	Q9BPA7	Q9bpa7 conus texti
300	7	2.4	1639	13	Q8Q4W6	Q8q4w6 fugu rubrip	373	6	2.1	76	10	Q9ZTA6	Q9zta6 hordeum vul
301	7	2.4	2110	3	Q8X1E9	Q8xie9 emericella	374	6	2.1	76	10	Q91FF0	Q91ff0 arabidopsis
302	7	2.4	2370	16	Q82RE3	Q82re3 streptomyce	375	6	2.1	76	16	Q8E8Q1	Q8e8q1 shewanella
303	7	2.4	2479	11	Q63002	Q63002 rattus norv	376	6	2.1	77	5	Q9BPC7	Q9bpc7 conus ventr
304	7	2.4	2491	4	Q96PT5	Q96pt5 homo sapien	377	6	2.1	77	5	Q9BPA6	Q9bpa6 conus penna
305	7	2.4	2491	4	Q9Z7G9	Q9z7g9 homo sapien	378	6	2.1	77	5	Q9BPC2	Q9bpc2 conus ventr
306	7	2.4	3898	12	Q8Q8A0	Q8q8a0 bovine vira	379	6	2.1	77	5	Q9BPC8	Q9bpc8 conus ventr
307	7	2.4	4032	2	Q9WTF3	Q9wtf3 streptomyce	380	6	2.1	77	5	Q9BPC8	Q9bpc8 conus ventr
308	7	2.4	4197	12	Q8Q7Z8	Q8q7z8 bovine vira	381	6	2.1	77	16	Q88N08	Q88n08 pseudomonas

382	6	2.1	78	5	Q9BPB0	Q9bbp0 conus texti	455	6	2.1	108	16	Q9R6B5	Q9r6b5 agrobacteri
383	6	2.1	78	10	Q945D8	Q945d8 castanea sa	456	6	2.1	109	2	Q44379	Q44379 agrobacteri
384	6	2.1	78	17	Q927V0	Q927v0 sulfolobus	457	6	2.1	109	3	Q02613	Q02613 saccharomyc
385	6	2.1	79	5	Q9BPC5	Q9bpc5 conus ventr	458	6	2.1	109	16	Q8A671	Q8a671 bacteroides
386	6	2.1	79	10	Q39807	Q39807 glycine max	459	6	2.1	109	17	Q9VEB4	Q9yeb4 aeropyrum p
387	6	2.1	79	12	Q8JMS3	Q8jms3 mamestra co	460	6	2.1	110	2	Q8KVM2	Q8kvm2 aergeria sp
388	6	2.1	79	16	Q9EXU7	Q9exu7 rhizobium m	461	6	2.1	110	9	Q9T1B0	Q9t1b0 bacterioph
389	6	2.1	79	16	Q8Z107	Q8z107 salmonella	462	6	2.1	110	11	Q9CQ41	Q9cq41 mus musculu
390	6	2.1	80	4	Q9NS95	Q9ns95 homo sapien	463	6	2.1	110	16	Q8Y4Y9	Q8y4y9 listeria mo
391	6	2.1	80	5	Q9BPB8	Q9bpb8 conus penna	464	6	2.1	111	2	Q9A126	Q9a126 escherichia
392	6	2.1	80	16	Q8YY47	Q8yy47 anabaena sp	465	6	2.1	111	5	Q9V9E8	Q9v9e8 drosofila
393	6	2.1	80	16	Q8E404	Q8e404 streptococ	466	6	2.1	112	11	Q8CBW0	Q8cbw0 mus musculu
394	6	2.1	81	2	Q85908	Q85908 sphingomona	467	6	2.1	112	3	Q08498	Q08498 saccharomyc
395	6	2.1	81	5	Q9BHA0	Q9bha0 conus texti	468	6	2.1	113	10	Q81675	Q81675 leavenworth
396	6	2.1	81	12	Q9I4G2	Q9i4g2 sulfolobus	469	6	2.1	113	10	Q81674	Q81674 leavenworth
397	6	2.1	82	10	Q8L698	Q8l698 triticum ae	470	6	2.1	113	10	Q81673	Q81673 leavenworth
398	6	2.1	83	2	Q9XB44	Q9xb44 escherichia	471	6	2.1	113	16	Q83167	Q83167 tropheryna
399	6	2.1	84	2	Q34283	Q34283 yersinia pe	472	6	2.1	113	16	Q83FZ7	Q83fz7 tropheryna
400	6	2.1	84	12	Q55747	Q55747 chilo iride	473	6	2.1	113	16	Q7V5G4	Q7v5g4 tropheryna
401	6	2.1	85	2	Q9461	Q9461 mycoplasma	474	6	2.1	113	16	Q7U9D0	Q7u9d0 synechococ
402	6	2.1	85	16	Q9FPN9	Q9fpn9 cornebacte	475	6	2.1	114	16	Q9RK45	Q9rk45 streptomyce
403	6	2.1	85	17	Q9ZXF0	Q9zxf0 pyrobaculum	476	6	2.1	114	16	Q8A8U9	Q8a8u9 bacteroides
404	6	2.1	86	2	Q9Z641	Q9z641 mycobacteri	477	6	2.1	114	16	Q87RF3	Q87rf3 vibrio para
405	6	2.1	87	16	Q8XW88	Q8xw88 ralatonia s	478	6	2.1	115	16	Q839F9	Q839f9 enterococu
406	6	2.1	87	16	Q8P6G5	Q8p6g5 xanthomonas	479	6	2.1	115	16	Q81KC0	Q81kc0 bacillus an
407	6	2.1	88	16	Q8Y522	Q8y522 listeria mo	480	6	2.1	116	8	Q85D52	Q85d52 esox lucius
408	6	2.1	89	9	Q852Y9	Q852y9 mycobacteri	481	6	2.1	116	17	Q9VFM4	Q9vfm4 aeropyrum p
409	6	2.1	90	4	Q96FS8	Q96fs8 homo sapien	482	6	2.1	117	5	Q8IG02	Q8ig02 caenorhabdi
410	6	2.1	90	16	Q9RSN8	Q9rsn8 deinococcus	483	6	2.1	117	16	Q87CU7	Q87cu7 xylella fas
411	6	2.1	91	13	Q8UWJ2	Q8uwj2 gallus gall	484	6	2.1	117	16	Q87CA6	Q87ca6 xylella fas
412	6	2.1	91	16	Q9PCW8	Q9pcw8 xylella fas	485	6	2.1	118	5	Q16344	Q16344 caenorhabdi
413	6	2.1	92	2	Q45127	Q45127 bacillus ps	486	6	2.1	118	5	Q95PE0	Q95pe0 amblyomma a
414	6	2.1	93	16	Q8ZLJ8	Q8zlj8 streptomyce	487	6	2.1	118	15	Q40450	Q40450 human immun
415	6	2.1	94	11	Q9CF72	Q9cf72 mus musculu	488	6	2.1	118	16	Q92G60	Q92g60 rickettsia
416	6	2.1	95	16	Q88XN0	Q88xd0 lactobacill	489	6	2.1	119	11	Q8K477	Q8k477 rattus norv
417	6	2.1	95	16	Q833U5	Q833u5 enterococu	490	6	2.1	119	16	Q7WH73	Q7wh73 bordetella
418	6	2.1	96	16	Q83374	Q83374 escherichia	491	6	2.1	119	16	Q7W917	Q7w917 bordetella
419	6	2.1	97	1	Q9C4X1	Q9c4x1 sulfolobus	492	6	2.1	119	16	Q7VWP4	Q7vwp4 bordetella
420	6	2.1	97	6	Q8HIT7	Q8hit7 macaca mula	493	6	2.1	120	6	Q29206	Q29206 sus scrofa
421	6	2.1	97	6	Q8HXZ5	Q8hxz5 macaca mula	494	6	2.1	120	16	Q821J8	Q821j8 salmonella
422	6	2.1	97	16	Q98A16	Q98a16 rhizobium l	495	6	2.1	120	16	Q7UPT2	Q7upt2 rhodopirell
423	6	2.1	98	8	Q9G6Q5	Q9g6q5 diplophos t	496	6	2.1	121	16	Q9KMM1	Q9kmm1 vibrio chol
424	6	2.1	98	16	Q8YUJ3	Q8yu3 anabaena sp	497	6	2.1	122	2	Q49269	Q49269 mycoplasma
425	6	2.1	98	16	Q81RH9	Q81rh9 bacillus an	498	6	2.1	123	11	Q8BR67	Q8br67 mus musculu
426	6	2.1	99	9	Q8SCN5	Q8scn5 pseudomonas	499	6	2.1	123	11	Q8BR67	Q8br67 mus musculu
427	6	2.1	100	6	Q95MD5	Q95md5 bos taurus	500	6	2.1	124	11	Q8C614	Q8c614 mus musculu
428	6	2.1	100	12	Q9YU50	Q9yus0 turkey aden	501	6	2.1	124	16	Q87PE2	Q87pe2 vibrio para
429	6	2.1	100	16	Q8P6H9	Q8p6h9 xanthomonas	502	6	2.1	124	16	Q7UVZ5	Q7uvz5 rhodopirell
430	6	2.1	100	16	Q89V50	Q89v50 bradyrhizob	503	6	2.1	124	17	Q972R6	Q972r6 sulfolobus
431	6	2.1	100	16	Q9RPM3	Q9rpm3 salmonella	504	6	2.1	125	4	Q9NV40	Q9nv40 homo sapien
432	6	2.1	100	17	Q9CZ72	Q9cz72 sulfolobus	505	6	2.1	125	5	Q8WRC7	Q8wrc7 manduca sex
433	6	2.1	101	4	Q86YV5	Q86yv5 homo sapien	506	6	2.1	125	12	Q7TA18	Q7ta18 sars corona
434	6	2.1	101	11	Q91Z64	Q91z64 sigmodon hi	507	6	2.1	125	16	Q88BP3	Q88bp3 pseudomonas
435	6	2.1	101	16	Q9HV19	Q9hv19 pseudomonas	508	6	2.1	125	16	Q87QU9	Q87qu9 vibrio para
436	6	2.1	101	16	Q8ER14	Q8er14 oceanobacil	509	6	2.1	126	16	Q7U412	Q7u412 synechococ
437	6	2.1	102	4	Q9F1K8	Q9f1k8 homo sapien	510	6	2.1	127	4	Q9HBR3	Q9hbr3 homo sapien
438	6	2.1	102	11	Q8C3P2	Q8c3p2 mus musculu	511	6	2.1	127	6	Q04209	Q04209 ovis sp. ov
439	6	2.1	103	5	Q19451	Q19451 caenorhabdi	512	6	2.1	127	11	Q9CVR1	Q9cvr1 mus musculu
440	6	2.1	103	10	Q8S7P5	Q8s7p5 oryza sativ	513	6	2.1	127	16	Q92VJ9	Q92vj9 rhizobium m
441	6	2.1	104	2	Q7WWY1	Q7wwy1 alcaligenes	514	6	2.1	128	16	Q8D4D5	Q8d4d5 vibrio vuln
442	6	2.1	104	4	Q9H050	Q9h050 homo sapien	515	6	2.1	128	3	Q8XIY8	Q8xiy8 kluyveromyc
443	6	2.1	104	10	Q9XJ72	Q9xj72 cucumis sat	516	6	2.1	128	4	Q96SH5	Q96sh5 homo sapien
444	6	2.1	104	17	Q9YGB2	Q9ygb2 aeropyrum p	517	6	2.1	128	11	Q80ZT4	Q80zt4 mus musculu
445	6	2.1	105	6	Q9GLC5	Q9glc5 bos taurus	518	6	2.1	128	16	Q88P63	Q88p63 pseudomonas
446	6	2.1	106	3	Q9HE66	Q9he66 neurospora	519	6	2.1	129	11	Q8VP63	Q8vp63 pseudomonas
447	6	2.1	106	12	Q93359	Q93359 nicotiana t	520	6	2.1	129	16	Q912K6	Q912k6 pseudomonas
448	6	2.1	106	12	Q82001	Q82001 human papil	521	6	2.1	130	6	Q8EUF5	Q8euf5 mycoplasma
449	6	2.1	107	2	Q938S0	Q938s0 pseudomonas	522	6	2.1	130	10	Q9FK01	Q9fk01 arabidopsis
450	6	2.1	107	2	Q51606	Q51606 citrobacter	523	6	2.1	131	16	Q8PMB6	Q8pmb6 xanthomonas
451	6	2.1	107	6	Q8HXZ4	Q8hxz4 macaca mula	524	6	2.1	131	16	Q8PAL4	Q8pal4 xanthomonas
452	6	2.1	107	6	Q8HXZ3	Q8hxz3 macaca mula	525	6	2.1	132	4	Q75768	Q75768 homo sapien
453	6	2.1	108	2	Q49237	Q49237 mycoplasma	526	6	2.1	132	16	Q888F7	Q888f7 pseudomonas
454	6	2.1	108	10	Q8W0J8	Q8w0j8 oryza sativ	527	6	2.1	133	2	Q93F13	Q93f13 shigella fl

528	133	10	Q94KX8	Q94KX8 brassica na	601	151	11	Q9DA47	Q9da47 mus musculu
529	133	10	Q9S9F5	Q9s9f5 citrullus l	602	151	16	Q9ZQ16	Q9zq16 rhizobium m
530	133	16	Q99U85	Q99u85 staphylococ	603	151	16	Q8NTM9	Q8ntm9 corynebacte
531	134	17	Q9Y9B7	Q9y9b7 aeropyrum p	604	151	16	Q827S6	Q827s6 streptomyc
532	135	11	Q8BN36	Q8bn36 mus musculu	605	152	16	Q8E9N9	Q8e9n9 shewanella
533	135	16	Q82RQ3	Q82rq3 streptomyc	606	153	4	Q8NFX0	Q8nfx0 homo sapien
534	136	5	Q8MOY5	Q8mry5 drosophila	607	153	4	Q8P004	Q8p004 homo sapien
535	136	6	Q8GLZ1	Q8glz1 macaca fasc	608	153	4	Q7Z4E5	Q7z4e5 homo sapien
536	137	2	Q939Y4	Q939y4 mycoplasma	609	153	7	Q9XRLS	Q9xr15 equus cabal
537	137	11	Q9CVL6	Q9cvl6 mus musculu	610	153	11	Q9CQZ0	Q9cqz0 mus musculu
538	137	11	Q9CSJ7	Q9csj7 mus musculu	611	153	13	Q42210	Q42210 necturus ma
539	137	16	Q81H29	Q81h29 bacillus ce	612	153	16	Q82RR6	Q82rr6 streptomyc
540	137	17	Q26321	Q26321 methanobact	613	154	2	Q8KNL0	Q8kn10 salmonella
541	138	5	Q95Y93	Q95y93 caenorhabdi	614	154	8	Q8MOD3	Q8mod3 amoebidium
542	138	16	Q8YR56	Q8yr56 anabaena sp	615	154	11	Q8BNQ0	Q8bnq0 mus musculu
543	139	2	Q8VIX9	Q8vix9 leptospira	616	154	11	Q8OYI9	Q8oyi9 mus musculu
544	139	2	Q8AEB5	Q8aes5 leptospira	617	154	16	Q9K0G1	Q9k0g1 neisseria m
545	139	4	Q8BSX3	Q8bsx3 homo sapien	618	156	5	P83387	P83387 caenorhabdi
546	139	4	Q86SX2	Q86sx2 homo sapien	619	156	16	Q9PL49	Q9pl49 chlamydia m
547	139	16	Q9RGF2	Q9rgf2 deinococcus	620	156	16	Q9JTL8	Q9jtl8 neisseria m
548	139	16	Q88J71	Q88j71 rhizobium l	621	156	16	Q8DEE8	Q8dee8 vibrio vuln
549	139	16	Q8KD00	Q8kd00 chlorobium	622	156	16	Q93IN7	Q93in7 salmonella
550	139	16	Q9S4G1	Q9s4g1 leptospira	623	156	16	Q82DQ2	Q82dq2 streptomyc
551	139	16	Q7V985	Q7v985 prochloroco	624	157	10	Q22480	Q22480 oryza sativ
552	140	2	Q93MGO	Q93mgo thioabacillu	625	158	4	Q9UN54	Q9un54 homo sapien
553	140	3	Q9Y8D2	Q9y8d2 cochllobolu	626	158	5	O02430	O02430 dirofilaria
554	140	16	Q98G74	Q98g74 rhizobium l	627	158	5	Q86SC1	Q86sc1 penaeus jap
555	140	16	Q68750	Q68750 versinia pe	628	158	16	Q8PAY5	Q8pay5 xanthomonas
556	140	16	Q934Y7	Q934y7 salmonella	629	160	2	Q9AG92	Q9ag92 bdellovibri
557	140	17	Q9YD09	Q9yd09 aeropyrum p	630	160	2	Q9EY90	Q9ey90 corynebacte
558	140	17	Q9HI77	Q9hi77 thermoplasm	631	160	2	Q9EUL3	Q9eul3 corynebacte
559	141	10	Q40849	Q40849 picea glauc	632	160	16	Q8ZK30	Q8zk30 salmonella
560	142	2	Q52137	Q52137 escherichia	633	160	16	Q8Z117	Q8z117 salmonella
561	142	2	Q9AJ18	Q9aj18 escherichia	634	161	10	Q9AY91	Q9ay91 oryza sativ
562	142	16	Q85634	Q85634 escherichia	635	162	10	Q9ZVG1	Q9zvg1 arabidopsis
563	142	17	Q58906	Q58906 pyrococcus	636	162	16	Q8EYI0	Q8eyi0 leptospira
564	143	4	Q9H7F1	Q9h7f1 homo sapien	637	162	16	Q8YTM3	Q8ym36 vibrio para
565	143	16	Q7UP01	Q7up01 rhodopirell	638	163	10	Q7Y0A1	Q7y0a1 oryza sativ
566	143	17	Q93721	Q93721 pyrobaculum	639	163	12	P87622	P87622 cowpox viru
567	144	2	Q49381	Q49381 mycoplasma	640	163	16	Q913W3	Q913w3 pseudomonas
568	144	10	Q93XN9	Q93xn9 solanum tub	641	163	16	Q8HVA1	Q8hva1 pseudomonas
569	144	10	Q84MQ8	Q84mq8 oryza sativ	642	163	16	Q8X9Z5	Q8x9z5 escherichia
570	144	10	Q84TB8	Q84tb8 oryza sativ	643	163	16	Q8ZPM3	Q8zpm3 rhizobium m
571	144	13	Q9W731	Q9w731 acipenser r	644	163	16	Q8ZSP5	Q8zsp5 streptococc
572	144	16	Q8KE32	Q8ke32 chlorobium	645	163	16	Q7UDS8	Q7uds8 shigella fl
573	144	16	Q8DDC2	Q8ddc2 vibrio vuln	646	163	16	Q7U9N8	Q7u9n8 synechococc
574	145	5	Q96353	Q96353 drosophila	647	164	8	Q7VAL9	Q7val9 chara vulga
575	145	13	Q8JJC4	Q8jjc4 anguilla ja	648	164	16	Q9KP91	Q9kp91 vibrio chol
576	145	16	Q8C7I1	Q8c7i1 staphylococ	649	164	16	Q9KDM2	Q9kdm2 bacillus ba
577	145	16	Q89QF9	Q89qf9 bradyrhizob	650	164	16	Q8ZIG2	Q8zig2 yersinia pe
578	146	3	Q8TFL6	Q8tf16 candida gla	651	164	16	Q87SR9	Q87sr9 vibrio para
579	146	10	Q7XAD0	Q7xad0 lycopersico	652	164	16	Q8Z9H6	Q8z9h6 salmonella
580	146	11	Q9D3B3	Q9d3b3 mus musculu	653	165	4	Q9UFX5	Q9ufx5 homo sapien
581	147	1	Q977T2	Q977t2 uncultured	654	165	11	Q8C5Z3	Q8c5z3 mus musculu
582	147	2	Q57241	Q57241 streptomyce	655	165	16	Q8ZKI0	Q8zki0 salmonella
583	147	10	Q8S0H7	Q8s0h7 oryza sativ	656	165	16	Q8Z1T7	Q8z1t7 salmonella
584	148	5	Q9V3J5	Q9v3j5 drosophila	657	165	16	Q8ZDZ7	Q8zdz7 streptomyc
585	148	5	Q86E71	Q86e71 schistosoma	658	166	10	Q9XIX6	Q9xix6 oryza sativ
586	148	10	Q9AT13	Q9at13 solanum tub	659	166	10	Q7XRE9	Q7xre9 oryza sativ
587	148	16	Q8PQ15	Q8pq15 xanthomonas	660	166	16	Q25397	Q25397 helicobacte
588	149	16	Q8EYU8	Q8eyus leptospira	661	166	16	Q8NQK4	Q8ngk4 corynebacte
589	150	2	Q9ZGK5	Q9zgk5 leptospira	662	166	16	Q8AJE9	Q8aje9 pseudomonas
590	150	4	Q85973	Q85973 homo sapien	663	167	5	Q9QZB0	Q9qze0 cryptospori
591	150	10	Q8H8W3	Q8h8w3 oryza sativ	664	167	8	O48256	O48256 demyus cyp
592	150	10	Q8H3B6	Q8h3b6 oryza sativ	665	167	12	Q91KX0	Q91kx0 japonese en
593	150	11	Q8C219	Q8c219 mus musculu	666	167	16	Q8YX42	Q8yx42 anabaena sp
594	151	2	P71490	P71490 methyloicr	667	168	8	O48255	O48255 demyus vau
595	151	5	Q9GP20	Q9gp20 globodera r	668	168	10	Q39475	Q39475 closterium
596	151	10	Q8M3G6	Q8m3g6 oryza sativ	669	168	10	Q8H0X5	Q8h0x5 arabidopsis
597	151	10	Q7XBU7	Q7xbu7 oryza sativ	670	168	10	Q8W480	Q8w480 arabidopsis
598	151	11	Q62488	Q62488 mus musculu	671	168	12	O11859	O11859 avian infec
599	151	11	Q925P0	Q925p0 rattus norv	672	168	12	O11858	O11858 avian infec
600	151	11	Q8C4X3	Q8c4x3 mus musculu	673	168	16	Q99VW4	Q99vw4 staphylococ

674	168	16	Q8NNU4	Q8nn14 corynebacte	747	6	2.1	179	5	Q8GH60	Q8gh60 dictyosteli
675	168	17	Q26967	Q26967 methanobact	748	6	2.1	179	16	Q7UW08	Q7uw08 rhodospirall
676	169	5	Q8MKM4	Q8mkM4 drosophila	749	6	2.1	180	5	Q7YX37	Q7yx37 caenorhabdi
677	169	10	Q8S6P9	Q8sp69 oryza sativ	750	6	2.1	181	13	Q8AY40	Q8ay40 oncorhynchu
678	170	7	Q82110	Q82110 gadus morhu	751	6	2.1	181	16	Q8E8P9	Q8ep89 shewanella
679	170	10	Q84MW9	Q84mw9 oryza sativ	752	6	2.1	181	16	Q8D1B3	Q8d1b3 versinia pe
680	170	11	Q8CFU1	Q8cpul mus musculu	753	6	2.1	181	16	Q87FW6	Q87fw6 vibrio para
681	170	16	Q7W9M5	Q7wn5 bordetella	754	6	2.1	181	16	Q7WH22	Q7wh22 bordetella
682	171	16	Q827F9	Q827f9 streptomyc	755	6	2.1	181	16	Q7WEO0	Q7wwo0 bordetella
683	172	5	Q81971	Q81971 plasmodium	756	6	2.1	182	10	Q3Z0Z9	Q3z0z9 arabidopsis
684	172	12	Q8VBN8	Q8vbn8 thogoto vir	757	6	2.1	182	16	Q8YFJ3	Q8yFj3 anabaena sp
685	172	12	Q8VBP0	Q8vbp0 thogoto vir	758	6	2.1	182	16	Q8YU75	Q8yu75 rhodospirall
686	172	12	Q8VBP3	Q8vbp3 thogoto vir	759	6	2.1	183	16	Q8YU75	Q8yu75 rhodospirall
687	172	12	Q8VBP1	Q8vbp1 thogoto vir	760	6	2.1	184	2	Q9PQB2	Q9pqb2 ureaplasma
688	172	12	Q8VBM6	Q8vbm6 thogoto vir	761	6	2.1	184	2	Q9FOS3	Q9fOs1 escherichia
689	172	12	Q8VBP2	Q8vbp2 thogoto vir	762	6	2.1	184	2	Q8Z970	Q8z970 bacillus sp
690	172	12	Q8VBN9	Q8vbn9 thogoto vir	763	6	2.1	184	2	Q9FOS2	Q9fOs2 escherichia
691	172	12	Q8VBN7	Q8vbn7 thogoto vir	764	6	2.1	184	2	Q84DV9	Q84dv9 escherichia
692	173	2	Q87662	Q87662 salmonella	765	6	2.1	184	2	Q84DV1	Q84dv1 escherichia
693	173	2	Q8ETA8	Q8eta8 corynebacte	766	6	2.1	184	2	Q84DV7	Q84dv7 escherichia
694	173	6	Q8SL17	Q8sl17 felis silve	767	6	2.1	184	2	Q84BP6	Q8lbp6 arabidopsis
695	173	16	Q8SL17	Q8sl17 escherichia	768	6	2.1	184	10	Q8LBP6	Q8lbp6 arabidopsis
696	173	16	Q83SN8	Q83sn8 shigella fl	769	6	2.1	185	10	Q7XKG5	Q7xkg5 oryza sativ
697	174	6	Q9GMZ9	Q9gmz9 felis silve	770	6	2.1	185	16	Q9PEZ5	Q9pez5 xyella fas
698	174	10	Q8GR11	Q8gr11 oryza sativ	771	6	2.1	185	16	Q88QX8	Q88qx8 mycoplasma
699	174	10	Q7XTP9	Q7xtf9 oryza sativ	772	6	2.1	185	16	Q82WB4	Q82wb4 nitrosomona
700	174	11	Q8CR26	Q8cr26 mus musculu	773	6	2.1	185	16	Q81QH7	Q81qh7 bacillus an
701	174	12	Q8J040	Q8j040 japanese en	774	6	2.1	185	16	Q81DI6	Q81di6 bacillus ce
702	174	12	Q8J039	Q8j039 japanese en	775	6	2.1	186	2	Q9SUN2	Q9eun2 corynebacte
703	174	12	Q8J041	Q8j041 japanese en	776	6	2.1	186	16	Q88FJ8	Q88fj8 pseudomonas
704	174	12	Q8J042	Q8j042 japanese en	777	6	2.1	186	16	Q7TX03	Q7tx03 pseudobacteri
705	174	12	Q8J045	Q8j045 japanese en	778	6	2.1	187	10	Q23132	Q23132 arabidopsis
706	174	12	Q8J044	Q8j044 japanese en	779	6	2.1	187	10	Q8LY37	Q8ly37 arabidopsis
707	174	12	Q8J043	Q8j043 japanese en	780	6	2.1	187	10	Q8LQH6	Q8lqh6 arabidopsis
708	174	12	Q80BF1	Q80bf1 japanese en	781	6	2.1	187	10	Q84S21	Q84s21 oryza sativ
709	174	12	Q80BF0	Q80bf0 japanese en	782	6	2.1	187	16	Q85857	Q85857 mycobacteri
710	174	12	Q80B39	Q80be9 japanese en	783	6	2.1	188	3	Q9HFA9	Q9hfa9 trichosporo
711	174	12	Q80B38	Q80be8 japanese en	784	6	2.1	188	10	Q9MCF1	Q9mcf1 bacteriopho
712	174	12	Q80BE7	Q80be7 japanese en	785	6	2.1	188	10	Q8LZW7	Q8lzw7 arabidopsis
713	174	12	Q80BE6	Q80be6 japanese en	786	6	2.1	188	16	Q9A5R3	Q9a5r3 caulobacter
714	174	12	Q80B35	Q80be5 japanese en	787	6	2.1	188	16	Q8X4T5	Q8x4t5 escherichia
715	174	12	Q80B34	Q80be4 japanese en	788	6	2.1	188	16	Q8AIP8	Q8aip8 pseudomonas
716	174	12	Q80B33	Q80be3 japanese en	789	6	2.1	188	16	Q88OX8	Q88ox8 pseudomonas
717	174	12	Q80B32	Q80be2 japanese en	790	6	2.1	188	16	Q82CS4	Q82cs4 streptomyc
718	174	12	Q80B31	Q80be1 japanese en	791	6	2.1	189	4	Q96EH4	Q96eh4 homo sapien
719	174	12	Q80B30	Q80be0 japanese en	792	6	2.1	189	12	Q9QBA8	Q9qba8 yaba monkey
720	174	12	Q80B29	Q80be9 japanese en	793	6	2.1	189	16	Q8XRMS	Q8xrm5 raistonia s
721	174	12	Q80B28	Q80be8 japanese en	794	6	2.1	189	16	Q8PI64	Q8pi64 xanthomonas
722	174	12	Q80B27	Q80be7 japanese en	795	6	2.1	190	6	Q7YR89	Q7ytr89 bos taurus
723	174	12	Q80B26	Q80be6 japanese en	796	6	2.1	190	10	Q8AX56	Q8ax56 oryza sativ
724	174	12	Q80B25	Q80be5 japanese en	797	6	2.1	190	10	Q7XBH6	Q7xbh6 oryza sativ
725	174	12	Q80B24	Q80be4 japanese en	798	6	2.1	190	12	Q9IGU8	Q9igu8 tanapox vir
726	174	16	Q8NQX6	Q8ngx6 corynebacte	799	6	2.1	190	16	Q8ZQ22	Q8zq22 salmonella
727	174	16	Q8CZ04	Q8czq4 versinia pe	800	6	2.1	192	2	Q70045	Q70045 escherichia
728	174	16	Q7ULY1	Q7uly1 mycobacteri	801	6	2.1	192	10	Q7XR59	Q7xr59 oryza sativ
729	175	2	Q8RPH8	Q8rfh8 erlichia r	802	6	2.1	192	13	Q9W733	Q9w733 acipenser r
730	175	6	Q81033	Q81033 bos taurus	803	6	2.1	192	16	Q8FIR6	Q8fir6 escherichia
731	176	16	Q8ZAD3	Q8zad3 versinia pe	804	6	2.1	192	16	Q8FIR6	Q8fir6 escherichia
732	176	16	Q8EHH1	Q8ehh1 shewanella	805	6	2.1	193	12	Q9EM12	Q9em12 bradyrhizob
733	176	16	Q7VAV3	Q7vaw3 prochloroco	806	6	2.1	193	16	Q97F15	Q97f15 clostridium
734	177	2	Q95QC3	Q95qc3 zymomonas m	807	6	2.1	193	16	Q9RFR9	Q9rfr9 deinococcus
735	177	4	Q86SM1	Q86sm1 homo sapien	808	6	2.1	194	2	P96080	P96080 thermus aqu
736	177	10	Q9C5U9	Q9c5u9 arabidopsis	809	6	2.1	194	10	Q8GRX6	Q8grx6 oryza sativ
737	177	10	Q8GVRS	Q8gvrs oryza sativ	810	6	2.1	195	2	Q9ZIW7	Q9ziw7 streptomyce
738	177	15	Q9IEB0	Q9iebo human immu	811	6	2.1	195	4	Q9UEF8	Q9uef8 homo sapien
739	177	16	Q8D6H0	Q8d6h0 vibrio vuln	812	6	2.1	195	10	Q9C9A5	Q9c9a5 arabidopsis
740	178	5	Q18959	Q18959 caenorhabdi	813	6	2.1	195	10	Q9C9A5	Q9c9a5 arabidopsis
741	178	16	Q92PF7	Q92pf7 thizobium p	814	6	2.1	195	10	Q22662	Q22662 arabidopsis
742	178	16	Q8ZBK1	Q8zbk1 versinia pe	815	6	2.1	195	12	Q9CQZ8	Q9cqz8 hyphantria
743	178	16	Q8FE49	Q8fe49 escherichia	816	6	2.1	195	16	Q92QX3	Q92qx3 rhizobium m
744	178	16	Q8DMP4	Q8dmp4 synectococc	817	6	2.1	195	16	Q81RX3	Q81rx3 bacillus an
745	178	16	Q87IR4	Q87ir4 vibrio para	818	6	2.1	196	11	Q7INK9	Q7tnk9 sciarus vul
746	178	17	Q96ZY3	Q96zy3 sulfolobus	819	6	2.1	196	12	Q9JFF7	Q9jff7 vaccinia vi

820	2.1	196	16	Q82Q52	streptomyc	893	6	2.1	211	16	Q8DCU3	Q8dcu3 vibrio vuln
821	2.1	197	10	Q7XP32	oryza sativ	894	6	2.1	211	16	Q81QF7	Q81qf7 bacillus ac
822	2.1	197	11	Q9JHG0	mus musculu	895	6	2.1	211	16	Q81DF7	Q81df7 bacillus ac
823	2.1	197	15	Q8Q2H0	Q8q2h0 caprine art	896	6	2.1	211	16	Q9KNX9	Q9knx9 vibrio chol
824	2.1	197	16	Q53706	Q53706 mycobacteri	897	6	2.1	212	2	Q9RPC9	Q9rpc9 streptomyc
825	2.1	197	16	Q7U256	Q7u256 mycobacteri	898	6	2.1	212	2	Q84CY3	Q84cy3 gamma-prote
826	2.1	197	17	Q8U272	Q8u272 pyrococcus	899	6	2.1	212	8	Q796Z5	Q796z5 russula ros
827	2.1	198	2	Q9F419	Q9f419 mycobacteri	900	6	2.1	212	10	Q9FTK1	Q9ftk1 oryza sativ
828	2.1	198	7	Q95HX1	Q95hxl peromyscus	901	6	2.1	212	16	Q9KC44	Q9kc44 bacilleria ha
829	2.1	198	8	Q7YB08	Q7yb08 rana sylvat	902	6	2.1	212	16	Q92FG4	Q92fg4 listeria in
830	2.1	198	8	Q7YB04	Q7yb04 rana clamit	903	6	2.1	212	16	Q9RT20	Q9rt20 deinococcus
831	2.1	198	8	Q7YB03	Q7yb03 rana septen	904	6	2.1	212	16	Q88Q17	Q88q17 pseudomonas
832	2.1	198	8	Q7YB02	Q7yb02 rana grylio	905	6	2.1	213	2	Q8G331	Q8gb31 pseudomonas
833	2.1	198	8	Q7YB01	Q7yb01 rana grylio	906	6	2.1	213	10	Q39156	Q39156 arabisdopsis
834	2.1	198	8	Q7Y827	Q7y827 rana septen	907	6	2.1	214	4	Q8T866	Q8tb86 homo sapien
835	2.1	198	8	Q7Y7M7	Q7y7m7 rana okaloo	908	6	2.1	214	10	Q8LW3	Q8liw3 oryza sativ
836	2.1	198	8	Q7Y7M6	Q7y7m6 rana clamit	909	6	2.1	214	10	Q8LN75	Q8ln75 oryza sativ
837	2.1	198	8	Q7Y7M5	Q7y7m5 rana okaloo	910	6	2.1	214	11	Q85W36	Q8bw36 mus musculu
838	2.1	198	8	Q7Y717	Q7y717 rana hecksc	911	6	2.1	214	16	Q7VE65	Q7ve65 prochloroco
839	2.1	198	10	Q4F210	Q4f210 arabisdopsis	912	6	2.1	215	6	Q81031	Q8i031 bos taurus
840	2.1	198	10	Q7T0A6	Q7t0a6 arabisdopsis	913	6	2.1	215	17	Q96Y57	Q96y57 sulfolobus
841	2.1	198	16	Q92KR4	Q92kr4 rhizobium m	914	6	2.1	216	4	Q43879	Q43879 homo sapien
842	2.1	198	16	Q8REL6	Q8rel6 fusbacteri	915	6	2.1	216	4	Q95220	Q95220 homo sapien
843	2.1	198	16	Q9R1W5	Q9riw5 streptomyc	916	6	2.1	216	10	Q9SUJ7	Q9suj7 arabisdopsis
844	2.1	199	4	Q3Y686	Q3y686 homo sapien	917	6	2.1	216	15	Q91E98	Q91e98 human immu
845	2.1	199	5	Q8MXR8	Q8mxr8 caenorhabdi	918	6	2.1	217	4	Q43888	Q43888 homo sapien
846	2.1	199	16	Q8D3Q2	Q8d3q2 vibrio vuln	919	6	2.1	217	4	Q00404	Q00404 homo sapien
847	2.1	200	4	Q3Y693	Q3y693 homo sapien	920	6	2.1	217	10	Q7XXF3	Q7xxf3 oryza sativ
848	2.1	200	10	Q9L171	Q9lt71 arabisdopsis	921	6	2.1	217	10	Q7XAV2	Q7xav2 lycopersico
849	2.1	200	10	Q84S22	Q84s22 oryza sativ	922	6	2.1	217	12	Q8V5Y9	Q8v5y9 bean pod mo
850	2.1	200	10	Q9FZK5	Q9fzk5 arabisdopsis	923	6	2.1	217	12	Q8V5Y7	Q8v5y7 bean pod mo
851	2.1	200	11	Q9D169	Q9d169 mus musculu	924	6	2.1	217	12	Q8V5Y5	Q8v5y5 bean pod mo
852	2.1	200	11	Q8BM86	Q8bm86 mus musculu	925	6	2.1	217	12	Q8V5Y8	Q8v5y8 bean pod mo
853	2.1	200	16	Q53746	Q53746 mycobacteri	926	6	2.1	217	12	Q8V5Y6	Q8v5y6 bean pod mo

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966 6 2.1 222 10 Q8LE41
967 6 2.1 222 10 Q93V72
968 6 2.1 222 10 Q8P927
969 6 2.1 222 16 Q87SR7
970 6 2.1 222 16 Q7VUL8
971 6 2.1 222 16 Q7U4R9
972 6 2.1 223 8 Q8WEU9
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974 6 2.1 223 8 Q8SR99
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977 6 2.1 224 2 Q87193
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979 6 2.1 224 8 Q8SRC7
980 6 2.1 224 8 Q8SRC3
981 6 2.1 224 8 Q8SRC1
982 6 2.1 224 8 Q8SRB5
983 6 2.1 224 10 Q89605
984 6 2.1 224 12 Q8Q0B1
985 6 2.1 224 16 Q88G00
986 6 2.1 225 8 Q8B513
987 6 2.1 225 8 Q8SRC9
988 6 2.1 225 8 Q8SRB7
989 6 2.1 225 8 Q8SRA5
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991 6 2.1 225 8 Q8SR87
992 6 2.1 225 16 Q81V49
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994 6 2.1 225 16 Q81DX0
995 6 2.1 226 2 Q8A154
996 6 2.1 226 5 Q82118
997 6 2.1 226 5 Q84935
998 6 2.1 226 8 Q8A06
999 6 2.1 226 8 Q8SRA9
1000 6 2.1 226 8 Q8SR70

O8LE41 arabidopsis
Q93V72 arabidopsis
Q8P927 xanthomonas
Q87SR7 vibrio para
Q7VUL8 bordetella
Q7U4R9 synecococc
Q8WEU9 lithophaga
Q8WEU1 psilunio li
Q8SR99 comephorus
Q8K4V8 mus musculus
Q87J13 vibrio para
Q87193 streptomyce
Q8UGB2 homo sapien
Q8SRC7 abysocottu
Q8SRC3 asprocottu
Q8SRC1 asprocottu
Q8SRB5 limnocottu
Q89605 arabidopsis
Q8Q0B1 anticarsia
Q88G00 rhiobium 1
Q8B513 tetodontop
Q8SRC9 abysocottu
Q8SRB7 cottinella
Q8SRA5 procottus j
Q8SRA1 comephorus
Q8SR87 paracottus
Q81V49 bacillus an
Q81HX7 bacillus ce
Q81DX0 bacillus ce
Q8A154 burkholderi
Q82118 caenorhabdi
Q84935 loligo peal
Q8A06 lampetra fl
Q8SRA9 limnocottus
Q8SR70 triglopsis

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ALIGNMENTS

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RESULT 1
Q726A6 PRELIMINARY; PRT; 290 AA.
AC Q726A6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Inhibitory receptor IREM1.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel
RT inhibitory receptor expressed by myeloid cells".
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY303545; AAP57942.1; -.
KW Receptor.
SQ SEQUENCE 290 AA; 32354 MW; E9D84A6B417AA99B CRC64;

Query Match 57.2%; Score 166; DB 4; Length 290;
Best Local Similarity 99.6%; Pred. No. 1.7e-166;
Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTLVLLFWLSGYSIATQITPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGV 120

RESULT 2
Q8NAF5 PRELIMINARY; PRT; 244 AA.
AC Q8NAF5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein FLJ35438.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Niinomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omuka Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092757; BAC03966.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein_1.
SQ SEQUENCE 244 AA; 26643 MW; 2C7C6EAD5F9C7FA5 CRC64;

Query Match 51.4%; Score 149; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPLLTLVLLFWLSGYSIATQITPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPLLTLVLLFWLSGYSIATQITPTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGV 120
DB 61 DCKILVKTSGSEQVKRDRVSIKDNQKRTFTVTMEDLMKTDADTYWCIGIEKTGNDLGV 120
QY 121 VQVITDPAVTOETSSSPTLTGHLDNR 149
DB 121 VQVITDPAVTOETSSSPTLTGHLDNR 149

RESULT 3
Q8TDQ1 PRELIMINARY; PRT; 290 AA.
AC Q8TDQ1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NK inhibitory receptor.

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GN NKIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Wan T., Zhang W., Cao X.;
RT "Novel human NK inhibitory receptor NKIR precursor.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251706; AAM19039.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001986; E:SPS_synth.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00104; E:SPS_SYNTHASE_1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 290 AA; 32395 MW; D14FC04A047AAD10 CRC64;
Query Match 47.2%; Score 137; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.5e-136;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPELLTYLLFWLSQYSIATQITPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
DB 1 MPELLTYLLFWLSQYSIATQITPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWR 60
QY 61 DCKILVKTSGSEQVYKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGV 120
DB 61 DCKILVKTSGSEQVYKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGV 120
QY 121 VQVITDPAVPTQETSS 137
DB 121 VQVITDPAVPTQETSS 137
RESULT 4
Q8N6D0 PRELIMINARY; PRT; 194 AA.
ID Q8N6D0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CRRF35 leukocyte immunoglobulin-like receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028199; AAK28199.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 194 AA; 21399 MW; 33B6AABE48F4FD6D CRC64;
Query Match 46.2%; Score 134; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 7.6e-133;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 GYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSE 74
DB 18 GYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSE 77
QY 75 VKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGVTVQVITDPAVPTQEE 134
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DB 78 VKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGVTVQVITDPAVPTQEE 137
QY 135 TSSSPILTGHHLN 148
DB 138 TSSSPILTGHHLN 151
RESULT 5
Q7Z7I5 PRELIMINARY; PRT; 293 AA.
ID Q7Z7I5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 1.
GN IREML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375480; AAP42152.1; -.
KW Receptor.
SQ SEQUENCE 293 AA; 32655 MW; 66EBEA2F8D3CF43E CRC64;
Query Match 41.4%; Score 120; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.9e-118;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 GYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSE 74
DB 18 GYSIATQITGPTTVNGLERGSLTVQCVYRSGWETYLKWCRCGAIWRDCKILVKTSGSE 77
QY 75 VKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGVTVQVITDPAVPTQEE 134
DB 78 VKRDVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGVTVQVITDPAVPTQEE 137
RESULT 6
Q7Z7I4 PRELIMINARY; PRT; 165 AA.
ID Q7Z7I4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 2.
GN IREM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RT "Molecular and functional characterization of IREM-1, a novel inhibitory receptor expressed by myeloid cells.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375481; AAP42153.1; -.
KW Receptor.
SQ SEQUENCE 165 AA; 18655 MW; F163D7D366063099 CRC64;
Query Match 24.5%; Score 71; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.4e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 79 RVSIKDNKQRTFTVTMEDLMKTDADTYWCGIEKTDNDLGVTVQVITDPAVPTQETSS 138
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Db 82 RVSIKDNQKRTFTVMTEDLMKTDADTYWCGIEKTDGLGVTVQVTDIPAPVQETSSS 141
QY 139 PTLTGHHLNDR 149
Db 142 PTLTGHHLNDR 152

RESULT 7
Q8IX40 PRELIMINARY; PRT; 201 AA.
AC Q8IX40;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TREMS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Colonna M.;
RT "Triggering receptor expressed on myeloid cells 5.";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF427618; AN86133.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 201 AA; 2268 MW; 2B8027A48B897CAF CRC64;

Query Match 3.4%; Score 10; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DRVSIKDNQK 87
Db 74 DRVSIKDNQK 83

RESULT 8
Q8N6D1 PRELIMINARY; PRT; 238 AA.
ID Q8N6D1;
AC Q8N6D1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CMRF35 leukocyte immunoglobulin-like receptor, CMRF35
DE antigen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028091; AAH28091.1; -.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 238 AA; 27020 MW; 1E7679BE434BB8B9 CRC64;

Query Match 3.4%; Score 10; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 DRVSIKDNQK 87
Db 74 DRVSIKDNQK 83
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Db 111 DRVSIKDNQK 120

RESULT 9
Q7WEKO PRELIMINARY; PRT; 472 AA.
ID Q7WEKO;
AC Q7WEKO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative exported protein.
GN B94635.
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12310271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.M., Temple L., James K., Bason N., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX60451; CAA34997.1; -.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51100 MW; F2B1B82BD7535DAC CRC64;

Query Match 3.1%; Score 9; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LLVAASILA 177
Db 10 LLVAASILA 18

RESULT 10
Q7W381 PRELIMINARY; PRT; 472 AA.
ID Q7W381;
AC Q7W381;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative exported protein.
GN BPP4165.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12310271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.M., Temple L., James K., Bason N., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Saunders M., Saunders R., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
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RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; EX640435; CAE39444.1; -.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51100 MW; F2B1B82B7535DAC CRC64;

  Query Match          3.1%; Score 9; DB 16; Length 472;
  Best Local Similarity 100.0%; Pred. No. 2;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 LLVAASLLA 177
Db 10 LLVAASLLA 18
|||||

RESULT 11
Q88CW3 PRELIMINARY; PRT; 545 AA.
AC Q88CW3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 22, Last annotation update)
DE P0684C02.5 protein.
GN P0684C02.5.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
RT clone:P0684C02.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AP003290; BAB89049.1; -.
DR Gramene; Q881L2; -.
SQ SEQUENCE 545 AA; 61682 MW; 938C253DF890919 CRC64;

  Query Match          3.1%; Score 9; DB 10; Length 545;
  Best Local Similarity 100.0%; Pred. No. 2.3;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 LLLVAASL 175
Db 12 LLLVAASL 20
|||||

RESULT 12
Q88CW3 PRELIMINARY; PRT; 1102 AA.
AC Q88CW3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Potassium efflux system protein KefA, putative.
GN P05067.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]_TaxID=160488;
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=125334463;
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapf E., Scanlan D., Tran K., Moazzes A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

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RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016793; AAN70632.1; -.
DR TIGR; PP5067; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR006685; MSion channel.
DR InterPro; IPR006686; MS_channel_dom.
DR InterPro; IPR006182; Ppantne_S.
DR Pfam; PF00924; MS_channel; I.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
DR PROSITE; PS01246; UPF0003; 1.
KW Complete proteome.
SQ SEQUENCE 1102 AA; 122371 MW; 294E962DA96A6F00 CRC64;

  Query Match          3.1%; Score 9; DB 16; Length 1102;
  Best Local Similarity 100.0%; Pred. No. 4.5;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TLYLLFWL 13
Db 712 TLYLLFWL 720
|||||

RESULT 13
Q7WTF2 PRELIMINARY; PRT; 3956 AA.
AC Q7WTF2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Nana4.
GN NANA4.
OS Streptomyces nanchangensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=204925;
RN [1]_TaxID=204925;
RP SEQUENCE FROM N.A.
RC STRAIN=NS3226;
RA Sun Y., Zhou X., Dong H., Tu G., Wang M., Wang B., Deng Z.;
RT "A Complete Gene Cluster from Streptomyces nanchangensis NS3226
RT Encoding Biosynthesis of the Polyether Ionophore Nanchangmycin.";
RL Chem. Biol. 10:431-441(2003).
DR EMBL; AF521085; AAP42858.1; -.
DR EMBL; AF521085; AAP42858.1; -.
SQ SEQUENCE 3956 AA; 413394 MW; B6D961763065F9BD CRC64;

  Query Match          3.1%; Score 9; DB 2; Length 3956;
  Best Local Similarity 100.0%; Pred. No. 15;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ASLTGAE 258
Db 727 ASLTGAE 735
|||||

RESULT 14
Q57313 PRELIMINARY; PRT; 149 AA.
AC Q57313;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Phospholipase A2 precursor.
GN PLA2-2.
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.

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OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Iijima N., Nasu Y., Takashima Y., Esaka M.;
RT "cDNA cloning and gene expression of phospholipase A2 isoform in the
RL hepatopancreas of red sea bream, Pagrus major.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009286; BAA23737.1; -
DR HSSP; P00593; 4BP2.
DR GO; GO:0003509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; Phoslip; 1.
DR PRINTS; PRC0389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 149 POTENTIAL.
SQ SEQUENCE 149 AA; 16905 MW; 21D1BDEF1E60A75D CRC64;

Query Match 2.8%; Score 8; DB 13; Length 149;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 LLLVAASL 175
Db 7 LLLVAASL 14

RESULT 15
QJUMTO
ID QJUMTO PRELIMINARY; PRT; 186 AA.
AC QJUMTO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE IRC1c protein.
GN IRC1C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Cantoni C., Biassoni R.;
RT "IRC1 isoforms.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010102; CAB52292.1; -
SQ SEQUENCE 186 AA; 20639 MW; 00D5E9379190EEEC CRC64;

Query Match 2.8%; Score 8; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 ASLLAWRM 180
Db 83 ASLLAWRM 90

Search completed: September 16, 2004, 12:56:58
Job time : 150 secs

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